

G G A C G C G T G G G T G C G A G G C G A A G G T G A C C G G G G A C C G A G C A T T T C A G A T C T G C T C G G T A G A
C T T G T G C G A C C A C C A C C A T G T T G G C T G C A A G G C T G G T G T G T C T C C G G A C A C T A C C T T C T A G G
G T T T T C C A C C A G C T T T T C A C A A G C C C C C C T T G T G A A G A A T T C C A T C A C A A G A A T A C
A T G G C T G T T A A C A C T A G C A T T A G C C A G G A A T A T G C C A C C A A A C A A G A A T T G G A T T C C G C G T G G G A
G A A C T G G C C A A G A A C T C A A A G G C C A G C A G T T G G A A C C A T C G A T G G A A A A A A T T T A A A A T
T A G C A G A T G G G A A G A T G G T T T G T T G C T G A G G G G C T C T G T T G G T C T T G A G C A T T T G T G C T
C T A T G C C T T G G G A C T G T C A A T G A G A T T G G A G C A T T A G A A A G G C T G A T T T T G C C T C A G T
A T G T C A A G A T G A A T T A C C T T C C A C C A T T A T G A C T A G C A G G G A G T T G G T T T A A C A G C T
T T G T C T G C C A T A G C A A T C A G C A G A A C G C C T G T T C T A T G A A C T T C A T G A T G A G G G C T C T G
G G T G A C A A T T T G G T G T A C C T T T G C A G C A C T G G T T G G A G C T G G A A T G C T G T A C G A T C A A T A C
C A T A T G A C C A G A C C C A G G C C C A A G A C A T C T G C T T G G T G T C A T A C T T T G G T G T A T G G G T
G C A G T G G T G G C T C C T C T G A C A A T A T A G G G G G T C C T C T T C T A T C A C A G C T G C A T G T G A T A C
A G C T G G C A T T T G T G G A G G C C T C T C C A C T G T G G C C A T G T G C G C C C A G T A A A A G T T C T G A
A C A T G G G T G C A C C C T G G G A G T G G C C T G G G T C T G C T T T G T G C C A T T G G G A T C T A T G
T T T C T T C A C C A C C A C C T G G T G T G T G C C A C T C T T A C T A C G T G C A A T G C A G G T G A C C G G T G A T
A G T T C T T T C A G A T G T C C T T C T G T A T G A T A C C C A A A G A T A A T C A A G G T G C A A G A T A C
A C C A A T G T A T G G A G T T C A A A A A T A T G A T C C C A T T A A C T C G A T G C T G A G T A T C T A C A T G G A T
A C A T T A A A T A T A T T A T G C G A G T T G C A A C T A T G C T G G C A A C T G G A G G C A A C A G A A A A T G C
A A G T A G C T C A G C T T C T G G C T C T C T G C T A C A T C A A A T A T C T G T T T A A T G G G G C A G A T A T G
A T T A A A T A G T T T G T A C A A C A G C T T T C G T T G A A G T T T A G A A G A T A A G A A A C A T G T C A T A T A
T T T A A A T G T C C G G T A A T G T A G T G C C T C A G G T C G C C T T T T T T C T G G A A A A T A A A T G C A T
A A T C C T C T C C C A A A T A A G C A C A C A C A T T T C A A T T C A T A T G T T G A G T A T T T T A A A A T G T T
T T G G T G A A T G T A A A A C T A A A G T T T G T G T C A T A G A A A T G A A G T C T T T T T C A T T T T A A A A
T T T A G T A G G T T C A C T A G T A A C T A A A A T T A G C A A A C T G T G T T G C A T A T T T T T T G A A G T
G C A A A T A T T G T A A T T A A T G T C A T A A G T A T T T G A G C T T T G G T A A A G G A C C A G A G A A G
G A G T C A C C T G C A G C T T T T T G T T T T T A A A A T C T A G A A C T A G C A C C T G T G T A T T G A T T A
G T A G A G G C C A G T A A G A A A C T T G G G A T T T G G A A C A A G T G G C A T T G T A C A T T C A T T T
G C T G A A C T T A A C A A A C T G T T C A T C T G A A A C A G C A C A G G T A G A T G A T C T C C T G C T G T T G
C T C T C A G T G C T C T T T C C A A T A T A G A T G G T G C A T G T T G A C T T G C A G A A T G T T A A C
A T A C A G A G A A T C C T T G A T G G A A T T A T A T A T G T G T G T T T A C T T T T G A A T G T T A C A A A A G G A A
A T A A C T T T A A A C T A T T C T A C A G A G A A A A T A T C A A A G C A T G A A A T A T G T T G C T T T T C C A G
A A T A C A A A C A G T A T A C T A G

FIGURE 2

MLAARLVCLRTLPSRVFHPAFTKASPVVKNSITKNQWLLTPSREYATKTRIGIRRGRTGQEL
KEAALEPSMEKIFKIDQMGRWVAVAGGAAGVGLGALCYGLGLSNEIGAIEKAVIWPQYVKDRI
HSTYMYLAGSIGLTALSAIAISRTPVLMNFMMRGSWVTIGVTFAMVGAGMLVRSIPYDQSP
GPKHLAWLLHSGVMGAVVAPLITILGGPLLIRAAWYTAGIVGGLSTVAMCAPSEKFLNMGAPL
GVGLGLVVFVSSLGSMFLPPTTVAGATLYSVAMYGGVLVLFMSMFLLYDTQKVIKRAEVS PMYGV
QKYDPINSMLSIYMDTLNIFMRVATMLATGGNRKK

[illegible]

FIGURE 4

MSDIGDWFRSIPAITRYWFAATVAVPLVGKLGSLSPAYLFLWPEAFLYRFQIWRPITATFYF
PVGPGTGFLYLVLNLYFLYQYSTRLETGAFDGRPADYLFMLLENWICIVITGLAMDMQLLMIP
LIMSVLYVWAQLNRDMIVSFWFGTRFKACYLPWVILGFNYIIGGSVINELIGNLVGHLYFFL
MFRYPMDLGGRNFLSTPQFLYRWLPSRRGGVSGFGVPPASMRRAADQNGGGGRHNWGQGFR
LDQ

Transmembrane domain:

amino acids 98-116, 152-172

N-myristoylation site.

amino acids 89-95, 168-174, 176-182, 215-221, 221-227, 237-243

Glycosaminoglycan attachment site.

amino acids 218-222

0990427 1140
10444 240660

FIGURE 5

GGGGCCGCGGTCTAGGGCGGCTACGTGTGTTGCCATAGCGACCATTTTGCATTAACGGTTG
 GTAGCTTCTATCCTGGGGGCTGAGCGACTGCGGGCCAGCTCTTCCCCTACTCCCTCTCGGCT
 CCTTGTGGCCCAAAGGCCTAACCGGGTCCGGCGGTCTGCGCTAGGGATCTTCCCGTTGCC
 CCTTTGGGGCGGG**ATGG**CTGCGGAAGAAGAAGACGAGGTGGAGTGGGTAGTGGAGAGCATCG
 CGGGGTTCTGCGAGGCCAGACTGGTCCATCCCCATCTTGGACTTTGTGGAACAGAAATGT
 GAAGTTAACTGCAAAGGAGGCATGTGATAACTCCAGGAAGCCCAGAGCCGGTGATTTTGGT
 GGCCTGTGTTCCCTTGTTTTTGTATGATGAAGAAGAAAGCAAATTGACCTATACAGAGATT
 ATCAGGAATACAAAGAACTAGTTGAAAAGCTGTTAGAAGTTACCTCAAAGAAATTGGAATT
 AATGAAGATCAATTTCAAGAAGCATGCACTTCTCCTCTTGCAAAGACCCATACATCACAGGC
 CATTTTGCAACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCCAGA
 AAAACATTGAAATGCAGCTGCAAGCCATTGGAATAATTCAAGAGAGAAATGGTGTATTACCT
 GACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAATCCT
 GAGGGAAGTTCTTAGAAAAATCAAAGAGGAATATGACCAGGAAGAAAGGAAGAGGAAAA
 AACAGTTATCAGAGGCTAAAACAGAAGAGCCACAGTGCATTTCCAGTGAAGCTGCAATAATG
 AATAATTTCCCAAGGGGATGGTGAACATTTTGACACCCACCCTCAGAAGTTAAATGCATTT
 TGCTAATCAGTCAATAGAACCTTTGGGAAGAAAAGTGAAAGGTCTGAAACTTCTCCCTCC
 CACAAAAAGGCCTGAAGATTCTTGGCTTAGAGCATGCGAGCATTGAAGGACCAATAGCAAAC
 TTATCAGTACTTGGACAGAGAAGAACTTCGGCAACGAGAACTATCTCAAGCAGAAGAGAGA
 TAAGTTGATGTCCATGAGAAAGGATATGAGGACTAAACAGATACAAAATATGGAGCAGAAAG
 GAAAACCCACTGGGGAGGTAGAGGAAATGACAGAGAAACCAGAAATGACAGCAGAGGAGAAG
 CAAACATTACTAAAGAGGAGATTGCTTGCAGAGAAACTCAAAGAAGAGTTATTATAAG**TA**
ATAATTAAGAACAATTTAACAAAATGGAAGTTCAAATTGTCTTAAAAATAAATTATTTAGTC
 CTTACACTG

FIGURE 6

MAAEEDDEVEWVVESIAGFLRGPDWSIPILDFVEQKCEVNCKGGHVITPGSPPEPVILVACVP
LVFDDEEESKLTYTEIHQEYKELVEKLLEGYLKEIGINEDQFQEACTIONSPPLAKTHTSQAILQP
VLAADFTIFKAMMVQKNIEMLQAIIRIIQERNGLVLPDCLTDGSDVVSDEHEEMKILREVL
RKSKEEYDQEEERKRKKQLSEAKTEEPTVHSSEAAIMNNSQGDGEHFAHPPSEVKMHFANQS
IEPLGRKVERSETSSLPQKGLKIPGLEHASIEGPIANLSVLGTEELRQREHYLKQKRDKLMS
MRKDMRTKQIQNMEQKGKPTGEVEEMTEKPEMTAEKQTLLKRRLLAEKLKEEVINK

N-glycosylation sites.

amino acids 224-228, 246-250, 285-289

N-myristoylation site.

amino acids 273-279

Amidation site.

amino acids 252-256

Cytosolic fatty-acid binding proteins.

amino acids 78-108

FIGURE 7

GGGCACAGCACATGTGAAGTTTTTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGAT
TCATCAGGAATACAAAGAAGCTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGGAA
TTAATGAAGATCAATTTCAAGAAGCATGCACTTCTCCTCTTGCAAAGACCCATACATCACAG
GCCATTTTGC AACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCC
AGAAAAACATTGAAATGCAGCTGCAAGCCATTGGAATAATTCAGAGAGAAATGGTGTATTA
CCTGACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAT
CCTGAGGGAAGTTCTTAGAAAATCAAAGAGGAATATGACCAGGAA

FIGURE 8

GCGTGGTTTTTTGTTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTCGCCTATACCTACTG
 TAGCTTCTCCACGTATGGACCCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTG
 TCTCAGCTCTAGGATGTGCGTTCTTCCACTAGAAAGCTCTCTGAGGGAGGTAATTAAGAAAC
 AGTGGAA**ATGG**AAAAACAGTGCTGTAGTCATCTCTGAATATGCTCCCTGTCAACAACTGATAC
 ATTCTCTGCTAGGTGCCATATTCTATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATT
 CTGCCAATGAAGAAAACAGTATGATTATCTTCCAACCTACTGTGAATGTGTGCTCAGAACTG
 GTGAAGCTAGTTTTCTGTGTGCTTGTGTCATCTGTGTTATAAAGAAAGATCATCAAAGTAG
 AAATTTGAAATATGCTTCTCTGGAAGGAATTTCTGTATTTCATGAAGTGGTCCATTCTCGCCT
 TTCTTTATTTCTGTGATAACTTGATTGCTTCTATGTCCTGTCCATCTTCAACCAGCCATG
 GCTGTTATCTTCTCAAATTTTAGCATTATAACAACAGCTCTTCTATTCCAGGATAGTGTGAA
 GAGGCGCTCAAACCTGGATCCAGTGGGCTTCCCTCCTGACTTTATTTTGTCTATTGTGGCCT
 TGACTGCCGGGACTAAAACCTTTACAGCACAACTTGGCAGGACGTGGATTTTCATCACGATGCC
 TTTTTCAGCCCTTCCAATTCCTGCCTTCTTTTCAGAAGTGAGTGTCCAGAAAAGACAATTG
 TACAGCAAAGGAATGGACTTTTCTGAAGCTAAATGGAACACCACAGCCAGAGTTTTCAGTC
 ACATCCGCTCTGGCATGGGCCATGTTCTTATTATAGTCCAGTGTTTATTCTTCAATGGCT
 AATATCTATAATGAAAGATACTGAAGGAGGGGAACAGCTCACTGAAAGCATCTTCATACA
 GAACAGCAAACTCTATTCTTTGGCATTCTGTTTAATGGGCTGACTCTGGGCCCTTCAGAGGA
 GTAACCGTGATCAGATTAAAGAACTGTGGATTTTTTATGGCCACAGTGCATTTTCAGTAGCC
 CTTATTTTGTAACTGCATTCCAGGGCCTTTCAGTGGCTTTTCATTCTGAAGTTCCCTGGATAA
 CATGTTCCATGCTCTTGATGGCCAGGTTACCACGTGCTATTATCACAAACAGTGTCTGTCTGG
 TCTTTGACTTCAGGCCCTCCCTGGAATTTTCTTGAAGCCCCATCAGTCTCTCTCTATA
 TTTATTTATAATGCCAGCAAGCCTCAAGTTCGGGAATACGCACCTAGGCCAAGAAAGGATCCG
 AGATCTAAGTGGCAATCTTTGGGAGCGTTCCAGTGGGGATGGAGAAGAACTAGAAAAGCTTA
 CCAAACCCAGAGTGATGAGTCAGATGAAGATACTTTCT**TA**ACTGGTACCCACATAGTTTGCA
 GCCTCTTGAACCTTATTTTTCACATTTTCAGTGTGTTGAATATTTATCTTTTCACTTTGATA
 AACCAGAAATGTTTCTAAATCCTAATATTCTTTGCATATATCTAGCTACTCCCTAAATGGTT
 CCATCCAAGGCTTAGAGTACCCAAAGGCTAAGAAATTTCAAAGAAGCTGATACAGGAGTAAAC
 ATATGAAGAATTCATTAATATCTCAGTACTTGATAAATCAGAAAGTTATATGTGCGAGATTAT
 TTTCTTGGCCTTCAAGCTTCCAAAAAAGCTTGTAAATATCATGTTAGCTATAGCTTGTATAT
 ACACATAGAGATCAATTTGCCAAATATTCACAATCATGTAGTCTTCTAGTTTACATGCCAAAGT
 TCTCCCTTTTAAACATTATAAAGCTAGGTTGTCTCTTGAATTTTGAAGCCCTAGAGATAGT
 CATTTTGTCAAGTAAAGAGCAACGGGACCCCTTCTAAAAACGTTGGTTGAAGGACCTAAATAC
 CTGGCCATACCATAGATTTTGGATGATGTAGTCTGTGCTAAATATTTTGTGTAAGAAGCAT
 TTCTCAGACACAACATCTCAGAATTTTAAATTTTGAAGAAATTCAGGAAATTTGGATTTTGT
 AATAATCTTTGATGTTTTAAACATTGGTTCCCTAGTACCATAGTTACCACCTTGTATTTTA
 AGTCATTTAAACAAGCCACGGTGGGGCTTTTTCTCCTCAGTTTGGAGGAAAAAATCTTGAT
 GTCATTACTCTGAATTATTACATTTTGGAGAATAAGAGGGCACTTTTATTTTATAGTTACT
 AATTCAAGCTGTGACTATTGTATATCTTTCCAAGAGTTGAATGCTGGCTTCAGAATCATAC
 CAGATTGTGAGTGAAGCTGATGCCTAGGAACCTTTAAAGGATCCCTTCAAAGAGTCACTT
 AGCAAAACACATGTGACTTTTAACTGATGATGAATATTAATCTCTAAAAATGAGAAGACC
 AGTAATATATAAGTCACTTTACAGTGTACTTACACCTTAAAGATGCATGGTATTTTTCATG
 GTATTTTGCATGCAGCCAGTTAACTCTCGTAGATAGAGAAGTCAGGTGATAGATGATATTAA
 AAATTAGCAACAAAGTGACTTGCTCAGGGTCATGCAGCTGGGTGATGATAGAAGATGGG
 CTTTAACTGGCAGGCCGTGATGTTTACAGACTACCATCTGATAAATATGAGCTTTATGGTGT
 CATTTCTCAGAAATTTATACATTTCTGCTCTCCTTCTCCTAAGTTTCATGCAGATGAATATA
 AGGTAATATACTATTATATAATTCATTGTGATATCCCAATAATATGACTGGCAAGAAATTG
 GTGGAAATTTGTAATTAATAATTTAAACCT

FIGURE 9

MEKQCCSHPVICSLSTMYTFLLGAIFFIALSSSRILLVKYSANEENKYDYLPTTVNVCSELVK
 LVFCVLVSFCVIKKDHQSRNLKYASWKEFSDFMKWSIPAFLYFLDNLIVFYVLSYLPAMAV
 IFSNFSIITTTALLFRIVLKRRLNWIQWASLLTLFLSIVALTAGTKTLQHNLAGRGFHHDAFF
 SPSNSCLLFRSECPRKDNCTAKEWTFPEAKWNTTARVFSHIRLGMGHVLIIVQCFISSMANI
 YNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRSNRDQIKNCGFFYGHSAFSVALI
 FVTAFQGLSVAFILKFLDNMFHVLMAQVTTVIITTVSVLVFDFRPSLEFFLEAPSVLLSIFI
 YNASKPQVPEYAPRQERIRDLSGNLWERSSGDGEELERLTTPKKSDESDETF

Transmembrane domains:

amino acids 16-36 (type II), 50-74, 147-168, 229-250, 271-293,
 298-318, 328-368

N-glycosylation sites.

amino acids 128-132, 204-208, 218-222, 374-378

Glycosaminoglycan attachment site.

amino acids 402-406

N-myristoylation sites.

amino acids 257-263, 275-281, 280-286, 284-290, 317-323

CGTGCCCTGCGCAATGGGTGTGCGGTCGCTTTTTCCCAATCCGGACGTAATCGTGGTTTTTG
TTCTGCAATAGCGGGCTTAGAGGGAGGGGCTTTTTCGCCTATACCTACTGTAGCTTCTCCAC
GTATGGACCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTGTCTCAGCTCTAG
GATGTGCGTCTCTCCACTAGAAGCTCTTCTGAGGGAGGTAATTA AAAACAGTGGAAATGGAA
AAACAGTGTCTAGTCACTCTGTAATATGCTCCTGTGCAACAATGTATACATTCTGCTAGG
TGCCATATTCAATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATCTGCCAATGAAG
AAAACAAGTATGATTATCTTCCAAC TACTGTGAATGTGTGCTCAGAACTGGTGAAGCTAGTT
TTCTGTGTGCTTGTGTCATTCTGTGTTATAAAGAAAGATCATCAAAGTAGAAATTTGAAATA
TGCTTCTCGGAAGGAATTCTCTGATTTCATGAAGTGGTCCATTCTCGCCTTTCTTTATTTCC
TGGATAACTTGATTGTCTTCTATGTCCTGTCCATCTTCAACCAGCCATGGCTGTTATCTTC
TCAAATTTTAGCATTATAACAACAGCTCTTCTATT CAGGATAGTGTGAAGAGGCGTCTAAA
CTGGATCCAGTGGGCTTCCCTCCTGACTTTATTTTTGTCTATTGTGGCCTTGACTGCCGGGA
CTAAACTTTA

FIGURE 11

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGCGGCTTGCTAGCGCGCGCGGCC
 GTGGCTAAGGCTGCTACGAAGCGAGCTTGGGAGGAGCAGCGGCCCTGCGGGGCGAGGAGCAT
 CCCGCTTACCAGGTCCCAAGCGGCGTGGCCCGCGGGTCATGGCCAAAGGAGAAGGCGCCGAG
 AGCGGCTCCGCGGCGGGGCTGCTACCCACCAGCATCCTCCAAAGCACTGAACGCCCGGCCCA
 GGTGAAGAAAGAACCGAAAAAGAAACAACAGTTGTCTGTTTGAACAAGCTTTGCTATG
 CACTTGGGGGAGCCCCCTACCAGGTGACGGGCTGTGCCCTGGGTTTCTTCTTCTCAGATCTAC
 CTATTG**ATG**TGGGCTCAGGTGGGCCCTTTCTCTGCCTCCATCATCCTGTTTGTGGGCCGAGC
 CTGGGATGCCATCACAGCCCCCTGGTGGGCTCTGCATCAGCAAAATCCCCCTGGACCTGCC
 TGGGTGCCTTATGCCCTGGATCATCTTCTCCACGCCCTGGCCGTCTATTGCCCTACTTCCTC
 ATCTGGTTTCGTGCCGACTTCCCACACGGCCAGACCTATTGGTACCTGCTTTTCTATTGCCCT
 CTTTGAACAATGCTCAGTGTTTCCATGTTCCTACTCGGCTCTCACCATGTTTCATCAGCA
 ACCGAGCAGACTGAGCGGGATTCTGCCACGCCCTATCGGATGACTGTGGAAGTGTGGGCAC
 AGTGCTGGGCACGGCGATCCAGGGACAAATCGTGGGCCAAGCAGACACGCCCTTGTTCAGG
 ACTTCAATAGCTCTACAGTAGCTTCACAAAGTGCCAACCATAACATGGCACCACTTTCACAC
 AGGGAACCGCAAAAGGCATACCTGCTGGCAGCGGGGCTATTGTCTGTATCTATATAATCTG
 TGCTGTCTATCCTGATCCTGGGCGTGGCGGAGCAGAGAGAACCCTATGAAGCCAGCAGTCTG
 AGCCAATCGCTACTTCCGGGGCTACGGCTGGTCATGAGCCACGGCCCATACATCAAACCTT
 ATTACTGGCTTCCTTTCACCTCCTTGGCTTTCATGCTGGTGGAGGGGAACCTTGTCTTGTT
 TTGCACCTACACCTTGGGCTTCCGCAATGAATCCAGAATCTACTCCTGGCCATCATGCTCT
 CGGCCACTTTAAACCATCCCATCTGGCAGTGGTTCTTGACCCGGTTTGGCAAGAAGACAGCT
 GTATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAA
 CCTCATATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGGCTTCTTAC
 TACCCTGGTCCATGTGCTGATGTGATTGACGACTTCCATCTGAAGCAGCCCCACTTCCAT
 GGAACCGAGCCCATCTTCTTCTCTTCTATGTCTTCTTCCAAAGTTTGCTCTGGAGTGTG
 ACTGGGCACTTTCTACCCTCAGTCTGGACTTGCAGGGTACCAGACCCGTGGCTGCTCGCAGC
 CGGAACGTGTCAAGTTTACACTGAACATGCTCGTGACCATGGCTCCCATAGTTCTCATCCTG
 CTGGGCTGCTGCTCTTCAAAATGTACCCATTGATGAGGAGAGGCGGCGGAGAAATAAGAA
 GGCCCTGCAGGCACTGAGGGACGAGGCCAGCAGCTCTGGCTGCTCAGAAACAGACTCCACAG
 AGCTGGCTAGCATCTCT**CTAG**GGCCCCGCCAGTTGCCCGAAGCCACCATGCAGAAGGCCACAG
 AAGGGATCAGGACCTGTCTGCCGGCTTGCTGAGCAGCTGGACTGCAGGTGCTAGGAAGGGAA
 CTGAAGACTCAAGGAGGTGGCCAGGACCTTGCTGTGCTCACTGTGGGGCCGGCTGCTCTG
 TGGCCTCCTGCTCCCCCTGCTGCTGTGGGCGCAAGCCCTGGGGCTGCCACTGTGAATA
 TGCCAAGGACTGATCGGCGCTAGCCCGGAACACTAGTGTAGAAACCTTTTTTTTACAGAGCC
 TAATTAATAACTTAATGACTGTGTACATAGCAATGTGTGTATGTATATGCTGTGAGCTA
 TTAATGTTATTAAATTTTCATAAAAGCTGGAAGC

09930427-111404

FIGURE 12

MWLRWALSLPPSSCLWAEFGMPSTPWWASASANPPGPAWVALCPGSSSPRPWPSLPTSSSG
SCPTSHRTARPIGTCFISIAKQWSRVSMFPTRLSPCSSATEQTERDSATAYRMTVEVLGTVL
GTAIQQQIVGQADTPCFQDFNSSTVASQSANHTHGTTSHRETQKAYLLAAGVIVICIYIICAV
ILILGVREQREPYEAQQSEPIAYFRGLRLVM SHGPYIKLITGFLTSLAFMLVEGNFVLFCT
YTLGFRNEFQNLLLAIMLSATLTIPIWQWFLTRFGKKTAVYVGISSAVPFLILVALMESNLI
ITYAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFHGTEPIFFSFYVFFTKFASGVSLG
ISTLSLDFAGYQTRGCSQPERVKFTLNMLVTMAPIVLILLGLLLFKMPIDEERRRQNKAL
QALRDEASSSGCSETDSTELASIL

FIGURE 13

GGGAAACGCAAAAGGCATACCTGCTGGCAGCGGGGTCATTGTCTGTATCTATATAATCTGT
GCTGTCATCCTGATCCTGGGCGTGCGGGAGCAGAGAGAACCCTATGAAGCCCAGCAGTCTGA
GCCAATCGCCTACTTCCGGGGCCTACGGCTGGTCATGAGCCACGGCCCATACATCAAACCTTA
TTACTGGCTTCCTCTTCACCTCCTTGGCTTTCATGCTGGTGGAGGGGAACCTTTGTCTTGTTT
TGCACCTACACCTTGGGCTTCGCAATGAATCCAGAATCTACTCCTGGCCATCATGCTCTC
GGCCACTTTAACCATTCCCATCTGGCAGTGGTTCTTGACCCGGTTTGGCAAGAAGACAGCTG
TATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAAC
CTCATCATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTACT
ACCTTGGTCCATGCTGCCTGATGTCATTGACGACTTCCATCTGAAGCAGCCCCACTTCCATG
GAACCGAGCCCAT

FIGURE 14

GGGGCTTCGGGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAGGTGCAGGT
 ATGAGCAGGCTCTGAAGACTAACATTTTGTGAAGTTGTAAAACAGAAAACCTGTTAGAAATG
 GGTGGTTTCAGCAAGGCCCTCAGTTTCCTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCT
 TTCATATTTTCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATAT
 CAGTGACACTGGTACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGG
 CAGTTTTATGCATTGCTACCATTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCTGAA
 GAGAACGTTATCATCAAATTAACAAGGCTGGCCTTGACTTGGAATACTGAGTTGTTTAGG
 ACTTTCATTGTGGCAAACCTCCAGAAAAACAACCCCTTTTGTCTGCACATGTAAGTGGAGCTG
 TGCTTACCTTTGGTATGGGCTCATTATATATGTTTGTTCAGACCATCTTTCCTACCAAATG
 CAGCCCAAATCCATGGCAAACAAGTCTTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGG
 AGTAAGTGCACCTTAGCATGCTGACTTGCTCATCAGTTTTGCACAGTGGCAATTTTGGGACTG
 ATTTAGAACAGAACTCCATTGGAACCCCGAGGACAAAGGTTATGTGCTTCACATGATCACT
 ACTGCAGCAGAATGGTCTATGTCATTTTCCTTCTTTGGTTTTTCTGACTTACATTGCTGA
 TTTTCAGAAAATTTCTTTACGGGTGGAAGCCAATTTACATGGATTAACCTCTATGACACTG
 CACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCCAGAGATATTGATGAAGGAT
 AAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAAGGTTACAGAAGTTGCTTA
 TTCTTCTCTGAAATTTTCAACCACTTAATCAAGGCTGACAGTAACACTGATGAATGCTGATA
 ATCAGGAAACATGAAAGAAGCCATTTGATAGATTATTCTAAAGGATATCATCAAGAAGACTA
 TTAAAAACACCTATGCCCTATACTTTTTTATCTCAGAAAAATAAGTCAAAAGACTATG

FIGURE 15

MWWFQQGLSFLPSALVIWTSAAFI FSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNI
AAVLCIATIIYVRYKQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSG
AVLTFGMGSLYMFVQTIILSYQMOPKIHGKQVFWIRLLLVIWCGVSALSMLTCSSVLHSGNFG
TDLEQKLHWNPEDKGYVLHMITTAAEWSMSFSFFGFFLTYYIRDFQKISLRVEANLHGLTLYD
TAPCPINNERTRLRSRDI

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FIGURE 16

CGGACGCTTGCGCNGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGTGCCTGATGCCGAGT
TCCGTCTCTCGGGTCTTTTCCCTGGTCCCAGGCCAAAGCGGAGCGGAGATCCTCAAACGGCCTA
GTGCTTCGCGCTTCCGGAGAAAATCAGCGGTCTAATTAATTCCTCTGGTTTGTTGAAGCAGT
TACCAAGAATCTTCAACCCTTTCCCACAAAAGCTAATTGAGTACACGTTCCCTGTTGAGTACA
CGTTCCTGTTGATTTACAAAAGGTGCAGGTATGAGCAGGTCTGAAGACTAACATTTTGTGAA
GTTGTAAAACAGAAAACCTGTTAGAAATGTGGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCT
TCAGCCCTTGTAATTTGGACATCTGCTGCTTTCATATTTTCATACATTACTGCAGTAACACT
CCACCATATAGACCCGGCTTTACCTTATATCAGTGACACTGGTACAGTANC

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FIGURE 17

CCCACGCGTCCGCCGCCGCTGCGTCCCGGAGTGCAGTGAGCTTCTCGGCTGCCCCGCGG
 CCGGGGTGCGGAGCCGACATGCGCCGCTTCTCGGCCCTCCTTCTGGTCTTCGCGGGTGCAC
 CTTGCGCTTGTACTTGTGTCGACGCGACTGCCCGCGGGCGGAGACTGGGCTCCACCGAGG
 AGGCTGGAGGCAGGTGCGTGTGGTTCCCCCTCCGACCTGGCAGAGCTGCGGGAGCTCTCTGAG
 GTCCTTCGAGAGTACCGGAAGGAGCACCAGGCCTACGTGTTCTCTGCTCTTCTGCGGCGCCTA
 CCTCTACAAACAGGGCTTTGCCATCCCCGGCTCCAGCTTCTCGAATGTTTTAGCTGGTGCCT
 TGTTTGGGCCATGGCTGGGGCTTCTGCTGTGCTGTGTGTTGACCTCGGTGGGTGCCACATGC
 TGCTACCTGCTCTCCAGTATTTTTGGCAAACAGTTGGTGGTGTCTACTTTCCTGATAAAGT
 GGCCCTGCTGCAGAGAAAGGTGGAGGAGAACAGAAACAGCTTGTTTTTTTTCTTATTGTTTT
 TGAGACTTTTCCCCATGACACCAAAGTGGTTCTTGAACCTCTCGGCCCCAATTCTGAACATT
 CCCATCGTGCAGTTCTTCTCTCAGTTCTTATCGGTTTGATCCCATATAATTTATCTGTGT
 GCAGACAGGGTCCATCTGTCAACCCTAACCTCTCTGGATGCTCTTTCTCTCTGGGACACTG
 TCTTTAAGCTGTTGGCCATTGCCATGGTGGCATTAAATTCCTGGAACCTCATTAATAAATTT
 AGTCAGAAACATCTGCAATTGAATGAACAAGTACTGCTAATCATATACACAGTAGAAAAGA
 CACATGATCTCGGATTTTCTGTTTGCCACATCCCTGGACTCAGTTGCTTATTTTGTAATGGA
 TGTGGTCTCTAAAGCCCCCATTGTTTTTGATTGCCCTTCTATAGGTGATGTGGACACTGTG
 CATCAATGTGCAGTGTCTTTTCAGAAAGGACACTCTGCTCTTGAAGGTGTATTACATCAGGT
 TTTCAAACCAGCCCTGGTGTAGCAGACACTGCAACAGATGCCTCCTAGAAAATGCTGTTTGT
 GGCCGGGCGCGGTGGCTCAGCCCTGTAATCCAGCACCTTGGGAGGCCGAGGCCGGTGATTCT
 ACAAGGTGAGGAGTTCAAGACCAGCTGGCCAAAGATGGTGAAATCCTGTCTCTAATAAAAAAT
 ACAAAAAATTAGCCAGGCGTGGTGGCAGGCACCTGTAATCCCAGCTACTCGGAGGCTGAGGC
 AGGAGAATTGCTTGAACCAAGGTGGCAGAGGTTGCAGTAAGCCAAGATCACACCACTGCACT
 CCAGCCTGGGTGATAGAGTGAGACACTGTCTTGAC

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FIGURE 18

MRPLLGLLLVFAGCTFALYLLSTRLPGRRLGSTEEAGGRSLWFPSDLAELRESEVLREYR
 KEHQAYVFLFCGAYLYKQGFaipgssflnVLagALFGPWLGLLLCCVLTsvGATCCYLLSS
 IFGKQLVVSYPDKVALLQRKVEENRNSLFFFLFLRLFPMTPNWFLNLSAPILNIPVQFF
 FSVLIGLIPYNFICVQTGSILSTLTSLDALFSWDTVFKLLAIAMVALIPGTLIKKFSQKHLQ
 LNETSTANHIHSRKDT

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domains:

amino acids 101-123, 189-211

N-glycosylation sites.

amino acids 172-176, 250-254

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 240-244, 261-265

N-myristoylation site.

amino acids 13-19, 104-110, 115-121, 204-210

Amidation site.

amino acids 27-31

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 4-15

Protein splicing proteins.

amino acids 25-31

Sugar transport proteins.

amino acids 162-172

CCGAGGCGGGAGGAGCCCGAGGGGGCGCGAGCCCGCATGAATCATTGTAGTCAATCATTTT
CCAGTTCTCAGCGCTCAGTTGTGATCAAGGGACACGTGGTTTCCGAACTGCCAGCTCAGAA
TAGGAAAATAACTTGGGATTTTATATTGGAAGACATGGATCTTGCTGCCAACGAGATCAGCA
TTTATGACAAACTTTCAGAGACTGTTGATTGTTGGTGAGACAGACCGGCCATCAGTGTGGCATG
TCAGAGAAGGCAATTGAAAAATTTATCAGACAGCTGCTGGAAAAAATGAACCTCAGAGACC
CCCCCGCAGTATCCTCTCCTTATAGTTGTGTATAAGGTTCTCGCAACCTTGGGATTAATCT
TGCTCACTGCCTACTTTGTGATTCAACCTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTCT
GGAGTCTCACACCTGGCGCTCACTCATCCATCACATTAGGCTGATGTCCTTGCCCATTGCCAA
GAGTACATGTCAGAAAATAAGGGATTTCTCTGCATGGGGGTGATGAAGACAGACCTTTC
CAGACTTTGACCCTGTGTGGACAAACGACATGTGAGCAGATGAGTCAGGCCATTCTTGCC
AACTGCACCTGGCTGTGCCAGAAACACCTGAAGGTGATGCTCCTGGAAGACGCCCCAAGGAA
ATTTGAGAGGCTCCATCCACTGGTGATCAAGACGGGAAGCCCTGTTGGAGGAAGAGATTC
AGCATTTTTTGTGCCAGTACCCTGAGGCGACAGAAGGCTTCTCTGAAGGGTTTTTCGCCAAG
TGGTGGCGCTGCTTTCCTGAGCGGTGGTTCCCATTTCTCTATCCATGGAGGAGACCTCTGAA
CAGATCACAAATGTTAGTGAGCTTTTTCTGTTTTCACTCACCTGCCATTTCCAAAAGATG
CCTCTTTAAACAAGTGCTCCTTCTTACCACAGAACCTGTGTGGGGAGTAAAGTGCATTAAG
ATGCCTGACCTATTTATCATTGGCAGCGGTGAGGCCATGTTGCAGCTCATCCCTCCCTTCCA
GTGCCGAAGACATTGTGAGTCTGTGGCCATGCCAATAGAGCCAGGGGATATCGGCTATGTG
ACCAACCCATCTGAAGGCTCTAGCTATTAGACAGAGGGGTCCAGCCTTTGGTCACTCTGCGAT
GGAACCGCTTTCTGGAAGCTGTAGGAAATAGCAGTGCACAGGAACAGTTCAGAGCCGA
AAACCAAGTTGAAAGGGGAAAAATAAAAACAAACAGTAAACTGCAAAAA

MDLAANEISISYDKLSETVDLVRQGTGHQCGMSEKATEKFIQRLLEKNEQRPFPFPYPLLIVVY
KVLATLGLILLTAYFVQIPFSPLAPEPVLSGAHTWRSLIHHIRLMSLP IAKKYMSENKGVP L
HGGDEDRPFPDFDPWWTNDCEQNESEPI PANCTGCAQXHLKVM LLEDAPRKFERLHPLV LKT
GKPLLEEEIQHFLCQYPEATEGESSEGFFAKWWRCFIPGWFFPFPY PWRRLNRSQMLRELFPV
ETHLPFVDDASLNKCSFLHPEFVGSGMKMKMDFLFI ISGSEAMLQLIPFPQRRHCQSVAMP
IEPQDIGVDTTHWKVYVIARGVQPLVLCGTAFSL

FIGURE 21

CCACGGTGTCCGTTCCTTCGCCCCGGCGGACAGCTGTCCCCGAGCGGGAGGAGCCCCAGGGGCG
CGAGCCCCGCATGAATCATTTAGTCAATCATTTCCAGTTCTCAGCCGTTCAAGTTGTGATC
AAGGGACACGTGGTTTCCGAACAGCTCAGATCAGAAATAGGAAATAACTTGGGATTTTATATT
GGAAGACATGGATCTTGCTGCCAACGAGATCAGCATTTATGACAACTTTAGAGACTGTTG
ATTTGGTGAGACAGACCGGCCATCAGTGTGGCATGTCAGAGAAGGCAATTGAAAAATTTATC
AGACAGCTGCTGAAAAGAATGAACCTCAGAGACCCCCCGAGTATCCTCTCCTTATAGT
TGTGTATAAGGTTCTCGCAACCTTGGGATTAATCTTGCTCACTGCCTACTTTGTGATTCAAC
CTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTGTGGAGCTCAC

FIGURE 22

CCCACGCGTCCGCCACGCGTCCGGCTGAACACCTCTTCTTTGGAGTCAGCCACTGATGAGG
 CAGGGTCCCCACTTGCAGCTGCAGAGCTGCAGAGCTGCAGAGCGCTGCTCCTGGCTGGT
 CCACTGGTGGCAGCTGCTAGACCGTGCCATGATGACGCGCTGGGCTGCACTGGGGATGCC
 CTCCTGCCACCCCAATGGCAGCCCACTTCTTTGAAGACTTCAGGACTTTTTGTGCCA
 CCCCAGTAATGGCCCACTTCATCGACAAACAGGTACAGCCAACTGTCAGGCTTGAATATG
 GACACGCTATGCTAAGAGCCAGCACTTATGTACGTTTCTGGAATGCTCTATGACATGCT
 TATGAGCACTGGGCTAGCGCCAGTGGGAGCGCGCCAGAGTCGTCGGGCTTCCAGGAGC
 TGGTGTCTGGAACCTTCGCGAGAGCGCGCGCGCTGGAGGGCTACGCTACACGGCAGTGTCTG
 AAGCAGCAGGCAACGCAGCACTCCATGGCCCTGCTGCAGTGGGGGGCGCTGTGGCGCCAGCT
 CGCCAGCCATGTGGGGCTGGGCGCTGAGGGACACTCCCATCCCCCGCTGGAAACTGTCCA
 GCCTCGAGACATATTCACGCTGGCTCTGAAGCTGGTGCCCAACCATCACTTCGACCTTCAC
 CTGGAAGCCAGCGCTCTCCGAGACAACTCTGGGTGAGGTTCCCTGACACCCACCGAGGAGGC
 CTCACCTGCTTGGCAGTGACCAAGAGGCCAAAGTAGCAGCCCAACCCAGTTGCTGCAGG
 AGGACAGCTCGGCGAGGACGAGCTGGCTGAGCTGGAGACCCGATGGAGGACGACGAACTG
 GATGAGCAGCTGAGAAGCTGGTCTGTCTGGCCGAGTGCCAGCTGGTGACGGTAGTGGCCGT
 GGTCCCAGGGCTGCTGGAGGTCAACACAGAAATGTATACTTCTACGATGGCAGCACTGAGC
 CGCTGGAACCCGAGGAGGGCATCGGCTATGATTTCCGCGCCCACTGGCCAGCTGCGTGAG
 GTCACCTTCGCGCTTTCAACTGCGCCGTTCAGCACTTGAGCTCTTCTTTATCGATCAGGC
 CAACTACTTCTCAACTTCCATGCAAGGTGGGACGACCCAGCTGCTACTCTCAGTACGAGA
 CTCGAGACCCAGCTGGCCCACTCCACCCCATACCCAGGTACGGAACCCAGGTGTACTCG
 TGGCTCTGCGCCTACGCGCCCTCTCAAGGCTACCTAAGAGCTACCTCCCGAGTTGCTGCAGG
 GCTGCGTGCTCAGGCCTTACCCAGAAATGGGTACAGGCTGAGATATCCAATCTCGAGTACT
 TGATGCACTCAACACCACTTTCGCGGGCGGAGCTACAACTGCTCTCAGTACCTGTGTCT
 CCTGGGTCTGACGAGTACTGTGCTCCCAACCTTGAGCTGACGACCCAGCGCTCTCCG
 GGACCTCTGAGCCCATCGGTGTGGTGAACCCCAAGCTGGCCAGCTGCTGAGGGAGAAGT
 ATGAAAGCTTTGAGGAGCCAGCAGGAGCAATGACAAGTTTCACTATGGCACCACCACTCC
 AATGACGAGCGCTGATGCACTACCTCATCCGCGTGGAGCCCTCACTCCCTGACGCTCCA
 GCTGCAAAAGTGGCCGCTTTGACTGCTCCGACCGGCGAGTTCACCTCGGTGGCGGAGCGCTGGC
 AGGCAGCCTGGAGGACCTGCCGATGTGAAGGAGCTCATCCCGAATTTCTTACTTTCTCT
 GACTTCTCTGGAGAACGACAGCGGTTTGAACCTGGGCTGTCTCCAGCTGACCAACGAGAAGGT
 AGGCGATGTGGTGCTACCCCGCTGGGCCAGCTCTCCTGAGGACTCATCCAGCAGCACCGCC
 AGGCTCTGGAGTCCGAGTATGTGTCTGCACACTACACGAGTGGATCGACTCATCTTTGGC
 TACAAGCAGCGGGGGCGAGCCGCGGAGGAGGCCCTCAATGTCTTCTATTACTGCACTTATGA
 GGGGGCTGTAGACCTGGACCATGTGACAGATGAGCGGGAACGGAAGGCTCTGGAGGGCATTA
 TCAGCAACTTTGGGCAAGTCCCTGTGACAGTGTGAAGGACCATCAACTCGGCTCTCA
 GCTGGAGGAAGCAGCCCATCGCTTGCACGCTTGGACACTAAGTCACTAGCATCTTCCAGCA
 CCTGGAGCAACTCAAGGCACTTTCGACAGAGGTGACTGTGAGTGGCAGTGGGCTGCTGGGCA
 CCCACAGCTGGTTGCCCTATGACCGCAACATAAGCAACTACTTCAGCTCAGCAAGAGCCCC
 ACCATGGGACGCCACAAGCAGCAGCACTGCTGAGTGGCCGTGAGGTGCCAGGCACTGGTGT
 GAGTGGACAAGCACTGGCAGTGGCCCGGATGGAAGCTGCTATTGAGCGGTGGCCACTGGG
 ATGGACAGCTGGAGGTGACTGCACTACCCGCTGGCAAGCTGTTGAGCAGCTGAGCTGCCAC
 CTTGATGTAGTAACCTGCCCTGCACTGGACACTGTGGCATTACCTCATCTCAGGCTGCCG
 GGACACCACTGTCAGTGGTGTGGCGGCTCCTGAGTACGGGTGCTGTCACTAGGCGCTGGC
 CAAAGCTGTGCGAGTCTGATGAGGATGGGGCTGCACTGAGCTGTGTGGCCATCAGCACT
 GTGATGACATGGCTGTGCTGAGTCTGAGGATGGAAGTGAATCATACACATGTAGCGCG
 CGGACAGTTTGTAGGCGCACTACGGCTCTGGGTGCCACATTCCTTGGACCTATTTTCCACC
 TGGCATTTGGGTGCGGAGCCAGATTTGGTACAGAGCTCAGCGTGGGCAAGCTCCTGGGGCC
 CAGGTCACTACTCTTGCACCTGTATTCAGTCAATGGGAAGTTGCGGGCTTCACTGCCCT
 GGCAGAGCAGCTCAGCTGACGGTGACAGAGGACTTTGTGTTGGCTGGGCAAGCTCCTGGGGC
 CGCCCTGACATCTCCAACATAACACACTGCTCCCGGCCGCGCTCCTTTGGCCATGAAG
 GTGGCCATCCGACAGCTGGCCGTGACCAAGGAGCGCAGCCAGTGTGGTGGGCTGGAGGA
 TGGCAAGCTCATCTGCTGGTGGTGGCGGGGACGCCCTCTGAGGTGGCAGAGCAGGAGTTCGCGC
 GGAAGCTGTGGCGGTCTCGCGGCGCATTCCCAAGTGTCTCGGAGAGCAGGAATACAA
 CCTACTGAGGCGCGCTGAAGCTGGCCAGTCCGGCTGCTCGGGCCCGCCCGCCGAGGCGCTG
 GCCCGGAGGCCCCGCCAGAAAGTCCGCGGGAACACCCGGGTGGGCACTGGGAGGCTGA
 GCGGGGCCACCTGCCAGCTCAGGGATTGGCGGGCGATGTTACCCCTCAGGGATTGGCG
 GCGGGAAGTCCGCGCCCTCGCGGCTGAGGGGCGCCCTGAGGGCCAGCACTGGCGTCT

FIGURE 23

MSQFEMDTYAKSHDMLSGFWNACYDMLMSSGQRRQWERAQSRRAFQELVLEPAQRRARLEGL
 RYTAVLKQQATQHSMALLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMRLKLPN
 HHFDPHLEASALRDNLGEVPLTPTEEASLPLAVTKEAKVSTPPELLQEDQLGEDELALET
 MEAAELDEQREKLVLSAECQLVTVVAVVPGLEVTQTQNVYFYDGSTERVETEEGIGYDFRRP
 LAQLREVHLRRFNLRRSALELFFIDQANYFLNFPCKVGTTPVSSSPQTPRPQPPIPHPTQV
 RNQVYSWLLRLRPPSQGYLSSRSPQEMLRASGLTQKWVQREISNFEYLMQINTIAGRTYNDL
 SQYPVFPWVLQDYVSPTLDLSNPAVFRDLKPIGVVNPKHAQLVREKYESFEDPAGTIDKFH
 YGTHYSNAAGVMHYLIRVEPFTSLHVQLQSGRFDCSDRQFHSVAAAWQARLESPADVKE
 LIP EFFYFPDFLENQNGFDLGCLQLTNEKVGDVVLPWPASSPEDFIQQHRQALESEYVSAHLHEW
 IDLIFGYKQRGPAEEEEALNVFYCTYEGAVDLDHVTDERERKALEGIISNFGQTPCQLLKEP
 HPTRLSAEEAAHRLARLDTNSPSIFQHLDELKAFFAEVTVSASGLLGTHSWLPYDRNISNYF
 SFSKDPMTGSHKTQRLLSGPWPVPGSGVSGQALAVAPDGKLLFSGGHWGDSLRVTALPRGKLL
 SQLSCHLDVVTCLALDTCGIYLISGSRDTCMVWRLRHQGGLSVGLAPKPVQVLYGHGA
 AVS CVAISTELDMAVSGSEDGTVIIHTVRRGQFVAALRPLGATFPGPFIHLAGLSEGQIVVQSSA
 WERPGAQVITYSLHYLVNKGKLRASLPLAEQPTALTVTEDFVLLGTAQCALHILQLNTLLPAA
 PPLPMKVAIRSVAVTKERSHVLVGLLEDGKLIVVAGQPSEVRSSQFARKLWRSSRRISQVSS
 GETEYNPTAR

N-glycosylation site.

amino acids 677-681

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 985-989

Tyrosine kinase phosphorylation site.

amino acids 56-65, 367-376, 543-551

N-myristoylation site.

amino acids 61-67, 436-442, 604-610, 610-616, 664-670, 691-697,
 706-712, 711-717, 769-775, 785-791, 802-808, 820-826, 834-840,
 873-879, 912-918, 954-960

FIGURE 24

CGGACGCGTGGGCGGACGCGTGGGGGCTGTGAGAAAGTGCCAATAAATACATCATGCAACCC
 CACGGCCACCTTGTGAACCTCTCGTGCCAGGGCTGATGTGCGTCTTCCAGGGCTACTCAT
 CCAAAGGCCTAATCCAAGTTCTGTCTTCAATCTGCAAATCTATGGGGTCTGGGGCTCTTC
 TGGACCTTAAGTGGGTACTGGCCCTGGGCCAATGCGTCCCTCGCTGGAGCCTTTGCCTCCTT
 CTACTGGGCTTCCACAAGCCCCAGGACATCCCTACCTTCCCTTAATCTCTGCCTTCATCC
 GCACACTCCGTTACCACACTGGGTCATTGGCATTGGAGCCCTCATCTGACCTTTGTGCG
 ATAGCCCGGTCATCTTGGAGTATATTGACCACAAGCTCAGAGGAGTGAGAACCCTGTAGC
 CCGCTGCATCATGTGCTGTTTCAAGTGCTGCCTCTGGTGTCTGGAAAAATTTATCAAGTTCC
 TAAACCGCAATGCATACATCATGATCGCCATCTACGGGAAGAATTTCTGTGTCTCAGCCAAA
 AATGCGTTCATGCTACTCATGCGAAACATTGTGAGGGTGGTGTCTGGACAAAGTCACAGA
 CCTGTGCTGTTCTTTGGGAAGCTGTGTGGTGGTGGAGGCGTGGGGTCTGTCTCTCTTTT
 TTTTCTCCGGTCGCATCCCGGGCTGGGTAAAGACTTTAAGAGCCCCACCTCAACTATTAC
 TGGCTGCCCATCATGACCTCCATCTCTGGGGGCTTATGTCATCGCCAGCGGCTTCTTACGCGT
 TTTCGCATGTGTGGACACGCTCTTCTCTGCTTCTCTGGAAGACCTGGAGCGGAACAACG
 GTCCTCTGGACCGGCCCTACTACATGTCCAAGAGCCTTCTAAAGATTCTGGGCAAGAAGAAC
 GAGGCGCCCCCGGACAACAAGAAGAGGAAGAAGTGAAGCTCCGGCCCTGATCCAGGACTGC
 ACCCCACCCCCACCGTCCAGCCATCCAACCTCACTTCGCCTTACAGGTCTCCATTTTGTGGT
 AAAAAAAGTTTTAGGCCAGGCGCCGTGGCTCACGCCCTGTAATCCAACACTTTGAGAGGCTG
 AGCGGGGCGGATCACCTGAGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTGAAACCTCC
 GTCTCTATTAAAAATACAAAAATTAGCCGAGAGTGGTGGCATGCACCTGTCATCCAGCTAC
 TCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCGGGAGGCAGAGGTGTCAGTGAGCCGAGA
 TCGCGCCACTGCACCTCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAACAA
 AAAGATTTTATTAAAGATATTTGTTAAGTCT

FIGURE 25

RTRGRTRGGCEKVPINTSCNPTAHLVNSSCPGLMCVFQGYSSKGLIQRSVFNLQIYGVLG
WTLNWWLALGQCVLAGAFASFYWAFHKPQDIPTFFPLISAFIRTLRYHTGSLAFGALILTLVQ
IARVILEYIDHKLGRGVQNPVARCIMCCFKCCLWCLEKFIKFLNRRNAYIMIAIYGNFCVSAK
NAFMLLMRNIVRVVLDKVTDLLFFGKLLVVGGVGLSFFFFSGRIPGLGKDFKSPhLNYY
WLPIMTSILGAYVIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYYSKSLKILGKK
EAPPDNKKKK

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FIGURE 26

GAGTCTTGACCGCCGCCGGGCTCTTGGTACCTCAGCGCGAGCGCCAGGCGTCCGGCCGCCGT
 GGCT**ATG**TTCTCGTGTCCGATTTCCGCAAAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCC
 TTCTCTTCGTGGCCTCGGACGTGGATGCTCTGTGTGCGTGCAAGATCCTTCAGGCTTGTTC
 CAGTGTGACCAAGTGCATATACGCTGGTTCCAGTTTCTGGTGGAAGAACTTGAAACTGC
 ATTCTTGAGCATAAAGAACAGTTTCATTATTTTATTCTCATAACTGTGGAGCTAATGTAG
 ACCTATTGGATATTCTTCAACCTGATGAAGACACTATATTCTTTGTGTGTGACTCCCATAGG
 CCAGTCAATGTCGTCATGTATACAACGATACCCAGATCAAATTACTCATTAAACAAGATGA
 TGACCTTGAAGTTCGCCCTATGAAGACATCTTCAGGGATGAAGAGGAGGATGAAGAGCATT
 CAGGAAATGACAGTGATGGGTGAGGCCTTCTGAGAAGCGCACACGGTTAGAAGAGGAGATA
 GTGGAGCAAACCATGCGGAGGAGGCGCGGCGAGAGTGGGAGGCCCGGAGAAGAGACATCCT
 CTTTGACTACGAGCAGTATGAATATCATGGGACATCGTCAGCCATGGTGATGTTTGAGCTGG
 CTTGGATGCTGTCCAAGGACCTGAATGACATGCTGTGGTGGGCCATCGTTGGACTAACAGAC
 CAGTGGGTGCAAGACAAGATCACTCAAATGAAATACGTGACTGATGTTGGTGTCTGACGCG
 CCACGTTTCCCGCCACAACACCGGAACGAGGATGAGGAGAACACACTCTCCGTGGACTGCA
 CACGGATCTCCTTTGAGTATGACCTCCGCCTGGTGCTCTACCAGCACTGGTCCCTCCATGAC
 AGCCTGTGCAACACCAGCTATACCGCAGCCAGGTTCAAGCTGTGGTCTGTGCATGGACAGAA
 GCGGCTCCAGGAGTTCCTTGACAGCATGGGTCTTCCCTGAAGCAGGTGAAGCAGAAGTTC
 AGGCCATGGACATCTCCTTGAAGGAGAATTTGCGGGAATGATTGAAGAGTCTGCAAATAAA
 TTTGGGATGAAGGACATGCGCGTGCAGACTTTCAGCATTCAATTTGGGTTCAAGCACAAGTT
 TCTGGCCAGCGACGTGGTCTTTGCCACCATGTCTTTGATGGAGAGCCCCGAGAAGGATGGCT
 CAGGGACAGATCACTTCATCCAGGCTCTGGACAGCCTCTCCAGGAGTAACCTGGACAAGCTG
 TACCATGGCCTGGAACTCGCCAAGAAGCAGCTGCGAGCCACCCAGCAGACCATTGCCAGCTGC
 CTTTGACCAACCTCGTCATCTCCAGGGGCTTTCTGTACTGCTCTCTCATGGAGGGCAC
 TCCAGATGTCATGTGTTCTCTAGGCCGGCATCCCTAAGCTGCTCAGCAAACACCTGCTCA
 AGTCCTTTGTGTGTTGCACAAAGAACCGCGCTGCAAACCTGCTGCCCTGGTGATGGCTGCC
 CCCCTGAGCATGGAGCATGGCACAGTGACCGTGGTGGGCATCCCCCAGAGACCGACAGCTC
 GGACAGGAAGAACTTTTTTGGGAGGGCGTTTGAGAAGGCAGCGAAAGCACCAGCTCCCGGA
 TGCTGCACAACCATTTTGACCTCTCAGTAATTGAGCTGAAAGCTGAGGATCGGAGCAAGTTT
 CTGGACGCACTTATTTCCCTCCTGTCC**TAG**GAATTTGATTCTTCCAGAATGACCTTCTTATT
 TATGTAACCTGGCTTTCATTAGATTGTAAGTTATGGACATGATTTGAGATGTAGAAGCCATT
 TTTTATTAAATAAAATGCTTATTTTAGGAAA

FIGURE 27

MFVSDFRKEFYEVVQSQRVLLFVASDVDALCACKILQALFQCDHVQYTLVPVSGWQELETAF
LEHKEQFHYFILINCGANVDLLDILQPEDETIFFVCDSHRPVNVNVYNDTQIKLLIKQDDD
LEVPAYEDIFRDEEEDEEHSGNDSGSEPSEKTRLEEEIVEQTMRRRQRREWEARRRDILF
DYEQYEHGTSSAMVMFELAWMLSKDLNDMLWWAIVGLTDQWVQDKITQMKYVTDVGVLRH
VSRHNRNEDEENTLSVDCTRISFEYDLRLVLYQHWSLHDSL CNTSYTAARFKLWSVHGQKR
LQEF LADMGLPLKQVKQKFQAMDISLKENLREMIEESANKFGMKDMRVQTF SIHFGFKHKFL
ASDVVFATMSLMESPEKDGSGTDHFIQALDSLRSNLDKLYHGLELAKKQLRATQQTIASCL
CTNLVISQGPFLYCSLMEGTPDVMLFSRPASLSLLSKHLLKSFVCSTKNRRCKLLPLVMAAP
LSMEHGTVTVVGIPPETDSSDRKNFFGRAFEKAAESTSSRMLHNHFDLSVIELKAEDRSKFL
DALISLLS

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GTACCTCAGCGCAGCGCCAGGCGTCCGGCCGCGTGCGTATGNTCGTGTCCGATTTCGCA
AAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCTTCTCTTCGTGGCCTCGGANGTGGAT
GCTCTGTGTGCGTGCAAGATCCTTCAGGCCCTGTTCAGTGTGACCANGTGCAATATANGCT
GGTTCCAGTTTCTGGGTGGCAAGAACTTGAACTGCATTCTTGAGCATAAAGAACAGTTTC
ATTATTTTATTCTCATAACTGTGGAGCTAATGTAGACCTATTGGATATTCTTCAACCTGAT
GAAGACCATATATTCTTTGTGTGTGACCCCATAGGCCAGTCAATGTTGTCAATGTATACAA
CGATACCC

FIGURE 29

CAGGAACCCCTCTCTTTGGGTCTGGATTGGGACCCCTTTCCAGTACCATTTTTTCTAGTGAAC
 CACGAAGGGACGATACCAGAAAACACCCTCAACCCAAAGGAAATAGACTACAGCCCCAATTG
 GCTGACTTTTGGCTATAGAAAAAGAAAGGAACGAAAAAGAGACAGTTTTTTTTGGAAAGCTAA
 GTCTTCCCTTTATCGAGTCAAGAAACCCCCCTTCTTGAGTATTTACAGCTTTTTAAACAATT
 GAGTAAAGTACGTCCTGGTCAAC**ATGG**TGACAGCGCCCTGGGTCCGCTTGGGACGGCTC
 CTGCTCTTTCTTCTGATGTGTGAGATCCGTATGTGGGAGCTCACCTTTGACAGAGCTGTGGC
 CAGCGGCTGCCAACGGTGCTGACTCTGAGGACCCCTGGATCCTGGCCATGTATCCTCTAG
 CCTCTTCTCCGGGCGCCCCACGGCCTGCTGAGATCAGACCTACATTAATATCACCATC
 CTGAAGGGTGACAAGGGGACCCAGGCCAATGGCCCTGGCAGGGTACATGGGCGAGGAGGG
 TCCCCAAGGGGAGCTTGGCCCTCAGGGCAGCAAGGGTGACAAGGGGAGATGGGCGAGCCCG
 GCGCCCGGTGCCAGAAGCGCTTCTTGGCTTCTCAGTGGGCGCCAGAGCGGCCCTGCACAGC
 GGGGAGGACTTCCAGACGTGCTCTTCAAGGGTCTTTGTGAACCTTGATGGGTGCTTTGA
 CATGGCGACCGGCAGTTTGGTGGCTCCCTGGCTGGCATCTACTTCTTCAAGCTCAATGTGC
 ACAGCTGGAATTACAGGAGACGTACGTGCACATTATGCATAACAGAAAGAGGCTGTCAATC
 CTGTACGCGCAGCCAGCGAGCGACGATCATGTCAGAGCCAGAGTGTGATCTGGACCTGGC
 CTACGGGGACCGCTCTGGGTGCGGCTCTTCAAGCGCCAGCGAGAACGCCATCTACAGCA
 ACGACTTCGACACCTACATCACCTTCAGCGGCCACCTCATCAAGGCCGAGGACGACT**GA**AGGG
 CCTCTGGGCCAGCTCCCGGCTGGAGAGCTCAGGTGGTCCCGTCCCTGCAGGGCTCAG
 TTTGCACTGCTGTGAGACGAGGAAGCCAGGGAGGTCCTCGGGACCTGGCATCTGGGAGAA
 CCTGCTTCTATCTTGGCTGCCATCATCCTCCAGGCTATTCTGCTCTCTCTCTCTCTCT
 TGGACCTATTCTAAACTTGCCTAACCTAAATATCTAGAACTTTCCGAGCCTCGTAGGCC
 AGCACTTTCTAAACTTGGAAATGCATCGAATCACCCGGGGTTCGPTTTAAATGCAGATTCT
 GACTCAGCAGTCTGAGTGGGTCCAGGATTCTGTCTTCTCATATGTTCTGGGTGATGCTG
 ATGGGTCAGTCTATGAACCACTCGAGCAACAGGTTCTAGGACTTTCTCAATATCTTAG
 TACTTTCTGAACATTCTGGAATCTCTCCCACTTCAGAATCTCCCAACATTTTTTTTTCT
 TGAGACAGAGTCTTGTCTGTGTGCCAGGCTAGAGTGCAGTGGTGCAATTCTAGTTCACTGC
 AACCTCTGCTTCCCGGTTCAAGCGATTCTCTGCTCCAGCTCCATGTGGCTGGGATTAC
 AGGCGCTGCTACCATGCTGCTGAATTTTTGTATTTTTAGTAGAGATGGGGTTCTCACATA
 TTGGCCAGGCTGGCTTTGAACCTCTGACTTCAGGTGACCCAGCCGCTTGGGCTCTCAAAAT
 GCTGGGATTACAGTGTGAGGCCACCGTGCTGGCCAAATCCAACTTTCTAAATTTCTCTCAT
 CCTCCAGGGCTCCCCGTGCTATGTTCTCTTTACCCCTTCCCCCTTCTCTTGTCTCAGGCC
 TGCAACCATGACCCACCGTTCATTTATTCATTATTAAACACTGAGCACTCACTCTGTGCT
 GGTCCTCGGGGAAGGGTGAGGGGTCAGACACAGGCCCTGCCCTGCCCTCAGTACTGGCCA
 GCTCCAGCCAGGCGGGGAGAGATGTGTACATAGGTTTTAAAGCAGCCAGGAGCTCATGGGG
 GCTCTGTGTTCTGGGTGTTTCAGGTGCTGTGGTCTCCATTAACCACTGCTCCCCAAGGCTGG
 TGGGACGGGTCCTGGTGGCAGGGGAGGTATCTCTTCCCGTTCCTCATCCACTGCCCCAG
 TGCTCATGCTTACAGCAAAACCCAGGGGCTTGGCCAGGTCAAGGGTTCTGTGAGGAGAGG
 ACCCAGGAGTGTGGGGCATTTGGGGGGTGAAGTGGCCCCGAAGATGGAACCCACACCCA
 TAGCTCTCCCAAGCTGATACGGCATCTGCGAGAAGACCTGCCCTCTCTCACTGGGATCCC
 CTTCCTGCTCTCTCCAGGGCTTGCAGGGGCTTGCTCAGTCCCTTCCACCAAGTCACTCT
 GAACCTCCGTTTTCCAGGGCTTCCAGTCTGCCCTCAGACACTGATGCTGTCCCCAGGTTGCT
 CTCTGCCCCCTCATGCCCCCTCTACCGGCCAGTGCCCCGACTCTCCAGGCTTTATCAAGGTG
 CTAAGGCCGGGTGGGCGAGTCTGCTCTCAGAGCCCTCTCCGGCTGGTGGCTGCCCTTTAC
 AAACACCTGCAAGGAGAAGGGCCACGGAAGCCCCAGGCTTTAGAGCCCTCAGCAGGTCTGGGG
 AGCTAGAGCAAGAGGAGGACTCAGGCCCTTCCGTTTCTTCTCCAGGGTGGGGTGGCTGGT
 GTTCCCCTAGCTCTCAAAACCCAGGTGGCTGCCCTTCTCCCCAGGGAGGAGGGCGGCCCTCCG
 CCATTGGTGCTCATGACTCTGGGCTGAGGTGCCCGGGGGTATCTCTGGTGCTCAC
 AGGCCAGGAGCCGCTGGCTCCATGGCCAGATGACGGAACAGGCTCTGACCAAGTGCCAGGA
 AGACCTGTGCTATAAACACCCCTGCCTGATCTGCCCTGACCCGCTGACCCGACGCCCTGCC
 GTCCAGCATGATTAAGAAATGCTGTCTCTTGGAAAAA

FIGURE 30

MVTAALGPVWAALLFLLMCEIRMVELTFDRAVASGCQRCCDSEDPLDPAHVSSASSSGRPH
ALPEIRPYINITILKGDGDPGPMGLPGYMGREGPGQGEFGQSGKDGEMGSPGAPCQKRF
FAFSVGRKTALHSGEDFQTLLEFRVFNLDGCFDMATGQFAAPLRGIYFFSLNVHSWNYKET
YVHIMHNQKEAVILYAQPSESRIMQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYIT
FSGHLIKAEDD

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 72-75

Clq domain proteins.

amino acids 144-178, 78-111 and 84-117

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ACTCGAACGCAAGTTCCTCGGGACCCAGGACCCCTCGGGCCGACCCGCCAGGAAAGACTG
 AGGCCCGCGCCCTGCCCGCCGGCTCCCTGCGCCGCGCCGCGCTCCCGGGACAGGAATGCTG
 CTCAGAGGTCCCTCTGCTGCTGCCGTGCTCTGCTATGCGCCTGGGCGCTGGGGTGCAGG
 GCTGCCCATCCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTTCTGCACTGCCCGCCAGGGG
 ACCACGGTGGCCCGAGACGCTGCCACCCGACAGGTGGGGCTTGACGTTCTTTGAGAACCGCAT
 CACCATGCTGCAGCAGCAGCACTTTGCGCGCTGCCGGGCTGCAGACTCTTGACACTTGCTAC
 AGAACAGATCGCCAGCACTGCCAGCGGGGTCTTCAGCCACCTGCACCACTCAGCAACCTG
 GACCTGACGGCCAAAGCTGCATGAATCACCATAAGACCTTCCGTGGCTCGCGCGCC
 CGAGCGCTCTACCTGGGCAAGAACCGCATCGCCACATCCAGCCTGGTGCTTCGACACGC
 TCGACCGCTCTCTGGAGCTCAAGCTGCAGAGCAACAGCTCGGGCAGCACTGCCCGCGCTGCGT
 TCGCCCGCGCTGCTGCTGCTGACCTCAGCCACACAGGCTCTTGGCTTCCAGCCCGGCAT
 CCTGGACATCGCCACCTGAGAGCGCTCGGCGCTGGCTGGTCTGGGGCTGCAGCAGCTGGACG
 AAGGGCTCTTCAGCGCTTGCGCACCTCCAGCACTGGATGTGTCCGACAACTAGCTGGAG
 CGAGTGCACTGTATCCGAGGCTCCGGGGCTGACGCGCTCGGGCTGGCCGCGCAACAC
 CCGATTCGCCAGCTCGGCCCGGAGCACTGGCCGACCTTGGCTGCCCTGACGAGGACTGGATG
 TGAACAACCTAAGCTCGAGGCCGCTGCTGGCAGCTCTCGGGCTCTTCCCGCGCTCGCG
 CTGCTGGCAGCTGCCCGCAACCCCTTCAACTGCGTGTGCCCTCTGAGCTGGTTTGGCCCCTG
 GGTGCGCGAGAGCCAGCTGCACACTGGCCAGCCTCGAGGAGACGCGCTGCCACTTCCGCCCA
 AGACGCTGGCCGGCTGCTCTGGAAGCTTGACTACGCGCACTTGGTGGCCAGCCACCAAC
 ACCACAGCCACAGTGGCCACACAGCGCCCGTGTGCGGGAGCCCAAGCTTGTCTTCTTAG
 CTGGCTCTCACTGGCTTAGCCCCAGCGCCGCGCACTGAGGCCCGCCAGCTCCGCCCTCCA
 CTGCCCAACCGACTGTAGGGCTGTGCCCGACGCCAGGACTGCCACCGTCCACTGCCCT
 AATGGGGGACATGTCACCTGGGGACAGCGCACCACTGGCGTGTGTGGTCCCGAAGGCTT
 CACGGGCTGTACTGTGAGAGCCAGATGCGGAGGGGACAGCCGCAAGCCCTACACAGTCA
 CGCCGAGGCCACACGCTCCCTGACCTTGGCCATCGAGCCGCTGAGCCCCACCTCCCTGCGC
 GTGGGGCTGCAGCGCTACCTCCAGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTACCTA
 TCGCAACCTATCGGGCCCTGATAAGCGGCTGGTGACGCTGCAGTGCCTGCCCTGCTGCCCTG
 AGTACACGCTCACCAAGCTCGGCCCGCAACGCCACTTACTCCGTCTGTGATCATGCTTTGGGG
 CCGGGCGGGTGGCGGAGGGCGAGGAGGCTGCGGGGAGGGCCATACACCCCAAGCCGTCCA
 CTCCAACACAGCCCCAGTACCCAGGCCCGCGAGGGGCAACCTGCCCGCTCTCATTTGCGCCG
 CCGTGGCCGGGTGCTCTCGGCCGCGCTGCGTTCGGTGGGGGACGCTCATGTGTGCGCGCG
 GGGCGGCGCATGCGACAGCGGCTCAGGACAAGGCGAGGTGGGGCGAGGGCTGGGCCCT
 GGAATCGAGGGAAGTGAAGGTCCCTTGTGAGCCAGGCCCGAAGGCAACAGAGGGCGGTGGAG
 AGGCCCTGCCAGCGGCTGTAGTGTGAGGTGCCACTTACGGCTTCCAGGGCTCTGGCCTC
 CAGTCAACCCTCCAGCGAAAGCCCTACATCT**TAGG**CCAGAGAGAGAGGCGAGCTGGGGCG
 GGCTCTCAGCCAGCTGAGATGGCCAGCCCTCTGCTGCCACACCACTGAGTTCTTCAGTGC
 CAACCTCGGGGATGTGTGCAGACAGGGTGTGTGACCACAGCTGGGCCGTGTTCCTCTGGA
 CCTCGGTCTCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCCAGAAC
 CGAGTGCCCTATGAGGACAGTGTCCGCGCTGCCCTCCGCAAGCTGCAGTCCCTGGGACCGCG
 GCGCTGCCATGTGCTGTGAACGATGCTGGTCTGCTGGGCTTCCCACTCAGCGGGA
 CCTGTGGGGCCAGTGAAGGAAGTCCCGGAAGAAGCAGGAGGAGCGGTTAGCGCGCTTTA
 TGACTCTAGTCTTGGCCCGAGGAAGCGAAGGAACAAAGAAACTGGAAGGAAGATGCTTTA
 GGAACATGTTTTGCTTTTTTAAATATATATATTTATAAGAGATCCTTCCCATTTATTCG
 GGAAGATGTATTTCAACTCAGAGCAAGGACTTGGTTTTTGTATAGACAACCATGATATG
 AAGGCGTTTTTGCAAAAAATAAAGATGAAGTGTGAAA

MCSRVPFLLLPLLLLALGPGVQCPSGQCQSQPQTVFCTARQGTTVPRDVPFDTVGLYVFEN
GITMLDAGSFAGLPGLQLLDLSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETFRGLR
RLERLYLGKNRIRHIQPGAFDTLDRLELKLQDNELRALPPLRLPRLLLLDLSHNSLLALEP
GILDTANVEALRLAGLGLQQLDEGLFSRLRNLHDLDSVDNQLERVPPVIRGLRGLTRLRLAG
NTRIAQLRPEDLAGLAAQLQELDVSNLSLQALPGDLSGLFPRLRLAAARNPFNCVCPLSWFG
FWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALS
SSLAPTWLSPTAPATEAPSPSTAPPTVGPVPQPDCCPSTCLNGGTCHLGRHHLACLCEPE
GTGLYLCESQMGGQTRPSPTAVTTPRPPRSITLGEIEPVSTSLRVGLQRYLQGSSVQLRSLRL
FYTNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSCVMYGLPGPRVPEAAEAGEAHTPPA
VHSNHAPVTQAREGNLPLLIPALAAVLLAALAVGAACVVRGRMAGAAAQDKGVGPAG
PLELEGVKVPLEPGPKATEGGEALPSGSECEVPLMGFPFGGLOSPLHAKFYI

FIGURE 33

GAATCATCCACGCACCTGCAGCTCTGCTGAGAGAGTGAAGCCGTGGGGGTTTTGAGCTCAT
 CTTTCATCATTCATATGAGGAAATAAGTGGTAAAACTCCTTGGAAATCAAACTAGAGACTCCTCAG
 AAACTTACATATTTTGTAGTATTGTTATGACAGCAGAGGGTGATGCTCCAGAGCTGCCAG
 AAGAAAGGGAACTGATGACCAACTGCTCCAACATGCTCTAAGAAAGGTTCCCGCAGACTTG
 ACCCGACGCCAACAGCAGCATCTGGATTATCCTATAACCTCCTTTTCACTCCAGAGTTCAGA
 TTTTCATTCTGCTCCAACATGAGAGTTTGTATTCTATGCCATAACAGAAATCCACAGCTGG
 ATCTCAAACCTTTGAAATTTCAACAAGGAGTTAAGATATTAGATTGTCTAATAACAGACTG
 AAGAGTGTAACTTTGGTATTCTAGTGGCAGGTCTCAGAGTATTAGACTCTTCTCTTAAGTACT
 TGACACCATGCTTATCTGTGAGGAAGCTGGCAACATGTCACACCTGGAATCCTAGGTTTGA
 GTGGGGCAAATAACAAAATCAGATTTCAGAAAATTTGCTCATCTGCACTTAATACTGTG
 TTCTTAGGATTCAGAACTCTTCTCATTATGAAGAAGGTAGCCTGCCATCTTAACACAAC
 AAAACTGCACATTGTTTACCATGGACACAAATTTCTGGGTCTTTTGGGTATGGAATCA
 AGACTTCAAAAATATTAGAAATGACAAATATAGATGGCAAAGCCAATTTGTAAAGTATGAA
 ATGCAACGAAATCTTAGTTTGA AAAATGCTAAGACATCGGTTCTATGTCTTAATAAGATTGA
 TTTACTCTGGGACGACCTTTTCCCTTATCTTACAATTTGTTGGCATAACATCAGTGGAACT
 TTCAGATCCGAAATGTGACTTTTGGTGGTAAGGCTTATCTTGACCACAATTCATTGACTAC
 TCAAACTACTGTAATGAGAACTATAAAATTTGGAGCATGTACATTTCCAGAGTGTTTTACATTCA
 ACAGGATAAAATCTATTGCTTTTGAACAAAATGGACATAGAAAACCTTGACAATATCAAATG
 CACAAATGGCCACACATGCTTTTCCCAGATTATCCTACGAAATTCGAATTTAAATTTTGGC
 AATAATATCTTAAACAGACGAGTTGTTTAAAAGAACTATCCAATCGCTCTACTTGAACACT
 CATTTTGAATTTGCAATAAATGGAGACACTTTCTTTAGTAAGTTGCTGTATCTGCTCTCAG
 CCTTGGAACTCTGGATCTGAGTCAAAATCTATTACAACATAAAAATGATGAAATTTGCTCA
 TGCCAGAACTGTGGTCAATATGAATCTGTATACAATAAATTTGCTGATCTGCTCTCAG
 GTGCTTGCCCAAAGTATTCAAATCTGACCTTAAATTAACCAAATCAAACCTGTACCTTA
 AAGAGACTATTCTCTGATGGCTTACGAGAACATAATTTGCAATTTAAATTTTCTAAGTAT
 CTCCTTGGATGCAGTCAATTTCTAGTAGACTTTTCAGTTCTGAACATTGAAATGAACCTTACTT
 CAGCCCATCTCTGGATTTTGTTCAGAGCTGCCAGGAGTTAAAACCTCTAAATGCGGGAAGAA
 ATCCATTCCGGTGTACCTGTGAATTA AAAATTTTCATTTCAGCTTGAACATATTCAGAGGTC
 ATGATGGTTGGATGGTCAGATTATACACTGTGAATACCTTTAAACCTAAGGGGAACATG
 GTTAAAGAGCTTATCTCTCCAGAAATATCTTGCAACACAGCTCTGTTGATTGTACCACTTG
 TGGTTATTATGCTAGTTCTGGGGTTGGCTGTGGCTTCTGCTGTCTCCACTTTGATCTGCC
 TGGTATCTCAGGATGCTAGGTCAATGCACACAAACATGGCAGAGGTTAGGAAACAAACCCA
 AGAACAACCAAGAGAAAATGCCGATTCCAGCATTTATTTACATACAGTGAACATGATCTCT
 TGTGGTGAAGAATGAATTTGATCCCAATCTAGAGAAGGAAGATGGTTCTATCTGATTTGCT
 CTTTATGAAAGCTACTTTGACCTTGGCAAAAGCATTAGTGAAATATTGAAGCTTATTGA
 GAAAAGCTATAAGTCCATCTTTGTTTGTCTCCCACTTTGTCCAGAATGAGTGGTGCCATT
 ATGAATTTCTACTTTGGCCACCACAATCTCTTCCATGAAAATTTCTAGTATATAATATCTTATC
 TTTACTGGAACCCATCTCCATCTATTGCAATCCCACAGGTATCATATAACTGAAAGCTCTCTCT
 GGAAAAAAGGACATCTTGGAAATGGCCAAAGGATAGGCTAAATGTGGGCTTTTCTGGGCAA
 ACCCTCGAGCTGCTATTAAATGTTAATGTATTAGCCACCAGAGAAATGTATGAACCTCAGACA
 TTCACAGAGTTAAATGAAGAGTCTCGAGGTTCTACAATCTCTCTGATGAGAACAGATTGGTCT
ATAAAAATCCACAGTCTCTTGGGAAGTTGGGGACCACATACACTGTTGGGATGTACATTGATA
 CAACCTTTATGATGGCAATTTGACAAATTTATTAATAAAAAATGGTTATTCCTTCTATA
 TCAGTTTCTAGAAGGATTTCTAAGAAATGTATCCTATAGAAAACACCTTCAAGATTTATAAGG
 GCTTTATGAAAAAGGTGTTTCATCCAGGATTGTTTATGACATGAAAAATGTGGCAGGTGCG
 AGTGGCTCACTCTGTTAATCCAGCACTATGGGAGGCCAAGTGGGTGAGCCACGAGGTCAA
 GAGATGGAGACCATCTTGGCCAACATGGTGAACCCCTGTCTCTACTGAAATGACAAAATTA
 CTTGGGCGTATGTTGTCAGCCTGTAGTCCAGCATCTTGGGAGGCTGAGGCAGGAGAATCT
 GCTGAACCCGGGAGGTGGCAGTTGCACTGAGCTGAGCTGAGCCACTGCACTGAGCTGGT
 GACAGCGGAGACTCCATCTCAAAAAAAGAAAAAAGAAAAAATGAAAAACATCC
 TCATGGCCAAAAATAAGGTCTAATTCATAAATATAGTAAATATGTAATATAATATTA
 CATGCCACTAAAAAGATAAGGTAGCTGTATTTTCTGGTATGAAAAAACATATTAATAT
 GTTATAAATCTATTAGGTTGGTGCAAAACTAATTTGGTGGTTTGGCAATGGCAATGGTAA
 ATAAAAAGTAAAGAAATCTATACCAGATGATGTAACAGTGGTTTGGGTCTGGGAGGTGGA
 TTACAGGGAGCATTTGATTTCTATGTTGTGATTTCTATAATGTTGAATTTTGAATGA
 ATCTGTATTTCTTTATAAGTAGAAAAAAATAAGATAGTTTTTACAGCCT

FIGURE 34

MRLIRNIYIFCSIVMTAEGDAPELPEERELMTNCSNMSLRKVPADLT PATTTLDLSYNLLFQ
 LQSSDFHVSVKLRVLILCHNRIQQLDKTFEFNKELRYLDLSNNRLKSVTWYLLAGLRYLDL
 SFNDFDTMPICEEAGNMSHLEILGLSGAKIQKSDFKIAHLHLNTVFLGFRTLPHYEEGSLP
 ILNTTKLHIVLPMDTNFWVLLRDGIKTSKILEMTNIDGKSQFVSYEMQRNLSLENAKTSVLL
 LNKVDLLWDDLFLILQFVWHTSVEHFQIRNVTFGGKAYLDHNSFDYSNTVMRTIKLEHVHFR
 VFYIQQDKIYLLLTCKMDIENLTISNAQMPHMLFPNYPTKFQYLN FANNILTDELFKRTIQLP
 HLKTLILNGNKLETLSLVSCFANNTPLEHLDLSQNLQHKNDENC SWPETVVNMNLSYNKLS
 DSVFRCLPKSIQILD LNNNQIQTVPKETIHLMAIRELNIAFNFLTDLP GCSHFSRLSVLNIE
 MNFILSPSLDFVQSCQEVKTLNAGRNPF RCTCELKNFIQLETYSEVMMVGWSDSYTCEYPLN
 LRGTRLKDVHLHELSCNTALLIVTIVIMLVGLAVAFCLHFDLPWYLRMLGQCTQTWHRV
 RKTTQEQLKRNVRFAFISYSEHDSLWVKNELIPNLEKEDGSILICLYESYFDPGKSISENI
 VSFIEKSYKSIFVLSPNFVQNEWCHYEFYFAHHNLFHENS DHIILILLEPIPFYCIPTRYHK
 LKALLEKKAYLEWPKDRRKGLFWANLRAAINVNVLATREMYELQTFTELNEESRGSTISLM
 RTDCL

FIGURE 35

GGGGGCTTTCTTGGGCTTGCTGCTTGGAAACCTGCCTCCAAGGACCGGCCCTCGGAGGGGTCGCCGGGAAAGG
 GAGGGAAGAAGGAAGGGCGGGGCGGGCCCCCTGCGCCCCGCCCGCGCTCTGCGCGCCCTCTGCCGCCCGCG
 CCAGCCAGCCCGAGCCCGCGGGCGGGTCAACAGCGCAGCCAGCGCGCTCCCGCGCCAGCGCGCGCT
 CTGCTGTGCCCTGCGCCCTTGCCCCGCGCAGCTTCTGCGCCCGCAGCCCGCCCGCGCGCCCGGTGACCGTGA
 CCGCTGCTGGCGCGGGCGGAGCAGCGCAGTCTCCGCGCCGGGACCGCTACCCAGCGCTGGCCCTGGTGCTC
 CTGSCAGTGACCTTGGCGGGTGGAGGCCAGGGCGCAGCCCTCGAGGACCTGATTATTCGGGACGAGGAT
 CTGAGCGCGGGAGCCCTACTACGCGCGCCGAGCGCCGAGCTCTGAGACCTCTCTCCGCGCTGGCTCGCGGGG
 CCGGGGAGGAGTGGGAGCGCGCCCGCAGGAGCCAGCGCGCCCAAGGGGGCCACCAAGCCCAAGGAAGCTCCC
 AAGAGGAGAGGTGCGCTCGGAGCGCGCTCCACAGGTAAACACAGCAACAAAAAGTATTAGAAACCAAGAG
 CATCGAGGGAGACTCAACATCCAGCGCGGCATTAAATGAAAAATGATTTTATGACGAGCGTGGTGCGCGGGAAG
 AAATGACCTCCAGCAGTGGATTGAAGTGGATGCTCGGCGCCTGACCGAGATTCACTGGTGTCTCACTCAAGGGA
 GGAATCCCTCTGGCTGAGTGACTGGTGACATCCTATAAGGTCTAGTGAGCAATGACAGCCACAGTGGGT
 ACTGTTAAGAATGGATCTGGAGACATGATATTTGAGGGAACAGTGAGAGGAGATCCCTGTCTCAATGAGCT
 ACCGTCGCCATGGTGGCCGCTACATCCGCATAAACCTCAGTCTGGTTTGATAATGGGAGCATCTGCATGA
 GAATGGAGATCTCGGCTGCCACTCGCAGATCTCAATAATTTATATCACCGCCGGAACGAGATGACCACTCT
 GATGACCTGGATTAAAGCAACAATTAAAGGAATGCGCCAGTTGATGAAGTTGTGAATGAAATGTGCTTCC
 CAATATCACCAGAAATTTACAACTTGAAAAAGCCACCGAGGCTGAGCTGTATGCTGTGGAGATCTGCAGAT
 ACCCTGGGAGCATGAAGTCTGTGAGCCGAGTTCCACTACATCGCGGGGCCCGCGCAATGAGTGTCTGGG
 CGGAGCTGCTGCTGCTGTGTCGAGTTCGTGTGTCAGGAGTACTGGCCGGAAATGCGCGCATCTGTCACCT
 GGTGGAGGAGCGCGGATTCACTCTCCCTCCCTCAACCCGAGTGGCTACGAGAAGGCTACGAGAAGGGGCT
 CGGAGCTGGGAGGCTGGTCCCTGGGACGCTGGAGCCACAGTGGAAATGACATCAACAACAACTTTCCGTATTTA
 AACACGCTGCTGGGAGCGAGGATCGACAGAATGTCCCGAGGAAGTTCCCAATCACTATATGATCTCC
 TGAGTGGTTCTGTGCGAAATGCCACGGTGGCTGCGGAGACAGAGCAGTCACTAGCCTGGATGCGAAAAATCC
 CTTTGTGTGCTGGGCGCAACTCGAGGGCGGAGCTGGTGGTGGCTATCCCTACGACTGTGCGGTGCCCT
 TGGAGAGCGTCAGGAACAACCCCGACCCCGGATGACCAGTGTTCGCTGGCTGGCTACTCTATGCTCCAC
 ACACCGCTCATGACAGACGCCCGAGGAGGTGTGCCACAGGAGACTTCCAGAGGAGAGGCACTGTCA
 ATGGGGCTCTGGGCAACCGTGCCTGGAAGTCTGAACGATTCACTACCTTCATACAACTGCTTGCAGACTG
 TCCATCTACGTGGGCTGTGATAAATACCCACATGAGAGCCAGCTGCCGAGGAGTGGGAGAAATACCGGAATC
 TCTGATCGTCTTATGAGCAGCTTCACTCTGGCATTAAAGGCTTGGTGAGAGATTACATGGAAAGGAATCC
 CAACCGCAATTATCTCCGTAGAAGGCATTAAACCATGACATCCGAAAGCAGCAAGTGGGATTAATGCGCGCT
 CTGAACCTGGAGATATGTGGTCAAGCAAGGCGAAGGTTTCACTGCATCCACAGAACTGTATGTGTG
 CTATGACATGGGCGCCAAAGTGTGACTTCACTTAGCAAAACCAATGCGGAGGATCCGAGAGATCATGG
 AGAAGTTTGGGAAGCAGCCCTGCCACTGCGCAGCGGCTGAAGCTGCGGGCGGAAGAGACGACAGCGT
 GGGTGAACCTCTGGGCGCTGAGACTCGCTGGGACCCATGCAAAATTAACCAACCTGGTAGTAGCTCCATAG
 TGGACTCTCACTCTGTTGTTCTCTGTAATCAAGAAGTGGCTGGAAGAGAGGTTGATTTGTGAGGCGAGTCC
 CAAAGGGAAGGCTGGAGGCTGAGGCTGTTTCTTTCTTTGTTGCCATTATCAAAATAACTGGACAGAGCA
 GCAGAGAAAGACTGAGGAGTGAGAGAACTCAGCAAGCAACCTGGGAATCAGAGAGAGAGGAGAGGAGG
 GAGGCTGCGCTGAGAGCTCTGGCTGCATAGAAAGGATTTGTTGCTCTCCCTCTTTGGTGGGACGAAG
 GTTCCAGTGCATTTGCAATTTGACACAGCTAAATTCAGCAATTTCCGAGCTGGGCTGTCCAAATGTACCA
 TTTGAGATGCTCCAGGCTCCTAAGAGAAATCCACCTCTCTGGCCCTGGGACATTGCAAGCTGCTCAAAATAA
 ATTCTGTGTTCTTTGACAAATAGCGTCAATGGCAAGTGACATCAGTGAAGCTCTTGAATCTGTTTATCTCT
 TTTTCAACAAAGGAGTGTGTGAGAAAGGAGAGAGGAGCTGAGATCACTCAGGAGTTTGTGGGACGAGCA
 TGGAGCTCTTGGCAAAATCTGGGCTCCATAAACAAACCCCAAGCTCTGCTGAGGTATTGCCCTGGAGGTT
 CCCAGGTAGGAGGAGCCAGAGTGCCAGCTCTCTGAAGGGCCAGAAATTTAGCTGGATCTCCTCTTTTAC
 CTGCTAGGACTGGAAAGAGCCGAGAGTGGGTGGCTGAAGCCCTCTCTGCTGTGAGGTATTGCCCTGTGTG
 GAATGTAGTGTCTATGGGTTGGCCTCATACAGCTGGGAGTTATTTTGATATGAGAAATGCCAGATCTTCA
 GATTAGGCTAAATGTAATGAAACCTTTAGGATTATCTGTGAGACATCAGTTGGGAGAAATTTGAATAT
 CTTGCAAGAAAAAGTATGTCTCACTTTTGTAAATGTGCTGCCTCATTGACCTGGGAAAAATGAAAAAAA
 AATAAGCAATGTGAAGACCTTAAAAA

FIGURE 36

MSRPGTATPALALVLLAVTLAGVGAQGALEDPPDYGQEIWSREPYARPEPELETFSPPPLP
 AGPGEEWERRPQEPRPPKRATKPKKAPKREKSAPEPPPPGKHSNKKVMRTKSSEKAANDDHS
 VRVAREDVRESCPLGLETLKITDFQLHASTVKRYGLGAHRGRLNIQAGINENDFYDGAWCA
 GRNDLQQWIEVDARRLRTFTGVITQGRNSLWLSDWVTSYKVMVSNDSHTWVTVKNGSGDMIF
 EGNSEKEIPVLNELFVPMVARYIRINPQSWFDNGSICMRMEILGCPLPDPNNYYHRRNEMTT
 TDDLDFKHHNYKEMRQLMKVVNEMCPNITRIYNIGKSHQGLKLYAVEISDHPGEHEVGEPEF
 HYIAGAHGNEVLGRELLLLLVQFVCQEYLARNARIVHLVEETRIHVLP SLNPDGYEKAYEGG
 SELGGWSLGRWTHDGDIDNNNFPDLNTLLWEAEDRQNVPRKVPNHYIAIPEWFLSENATVAA
 ETRAVIAWMEKIPFVLGGNLQGGELVVAYPYDLVRSPWKTQEHTPTPDDHVFRWLAYSYST
 HRLMTDARRRVCHTEDFQKEEGTVNGASWHTVAGSLNDFSYLHTNCFELSIYVGCDKYPHES
 QLPEEWENNRESLIVFMEQVHRGIKGLVRDSHGKGIPTNAIISVEGINHDIRTANDGDYWRLL
 NPGEYVVTAKAEGFTASTKNCMVGYDMGATRCDFTL SKTNMARI REIMEKFGKQPVSLPARR
 LKLRGRKRRQRG

TTAAGGACACAGCATAGAGCGGGCTCTCATTTCTCTAGCCCTCTCTGTCTTCTCTTCCGTGGCCAGCTGTCAGGGG
 ATTGTGGGGATCTGGGACCTCCAAATCCAGCCCGGGCTTCAGCTCTTCCAGAGTGTTGACTACAGCTCCAGG
 TTCAGCTCCAGCTCCAGGTGGGGCTCCAGCTTCAGCCGACAGCTTAGGACAGCGGAGTCTGTGTCCCACTGTGT
 TTTCCAAATTTCCACGGGCTCGTGAGTACGCTGGGACGTCGAGTGGCTGTGTTTCCCTGCGACAGCAACCTTT
 CCGTGGACAGAGATTGGAACGCTTGGAAATCGACATCATGTTCTTTCTCAGAAGTTTGAAGAAAGACTTTCTAA
 GTGAGGGAAATGTCCAAATTAATTAGTGTGATCGATAAAAGAAACTGTAAAGCTTAAGTCTCGGAATTGACATCAT
 GGAGAAGATGATACATTTTCTACATGCACTGGACTCGAGCTGATCAGAGTAGAAGTGAAGGAGATGGAAAAAT
 TGTGCTATACAGCTGAAGGAGATGTTTGTGGTAGAGCTCAGAAATTTGTGCACAGCTGGAGGTGGAGATGAAGAA
 ATGACTCTCTGTGTAGAGAAAGCTTGAGACATAGACAAAAAATTTGCTTGCATTCGCGGAGAAATCGTGGC
 TCTGAAGACAGAGCTGAAGAGTGTGAGGCTCTAAAGATCAAAACACCCCGTGTGCCACCTCTCCCACTC
 CAGGAGAGCTGTGCTATGTTGGTGTGGTGAACATGACAAACCGCTCTGTGTTGAGCTCAACTGGAGAGGGTTT
 TCTTATCTTATATGGTCTGGGGTAGGAGTATCTCCCGACATCAAAACAAAGGACTGTAATGGGTGGCGGCC
 ATTGAATACAGATGGGAGATCTGTGGAGATTATAGACTGTACACACATCGATGATTTGCTAATGTATATAAA
 ATGCTCGAGAGTTCGGGATCACTTATGGCCAGAGTAGTGTGATCAGAGTTTACAAACAACATCATGTACCTCAAC
 ATGTACACACACCGGGAATTTGCCAGAGTTAACTGACCACTGAACAGAGTTGGCTGTGATCAAACTCTCCCTAA
 TGTGCTCCTATATAACCGCTTTCTATATGCTTAATGTGCTTGGCAAGATATGACTTTGCTGTGGATGAGAATT
 GAGTCTGGGTTATTTTCTAACGTGAAGCGACATCGTGAACATGGTGATTTAGTAACCTCAATGACACACACTT
 CAGGTCGTAAACACTTGGTATACCAAGCAGTATAAAACACTTGCTTCAAGCCCTCATGGTATGTGGGGTCTCT
 GTATGCCACCGCTACTATGAACACAGACAGAGAAGAGATTTTATCTATTAGACACAAACAGGGAAGAGGG
 GCAAACTAGACATGTAAATGCATAAGATGACAGAAAGAACTGCAGAGCAATTAACATAAACCCCTTTGACCAAAA
 TCTTATCTCTATAAGTATGGTTACCTCTGAAATATGATCTTTCTGTCTGCGAGAAGCCAGTAAGCTGTTATA
 GGAATTAGGGTGAAGAGAGAAATTTGTGTGAAGAAATAGTCTCTCCACTTATAGATATCTCGAGGGGTCT
 CTAAGAAGTGTTCTATTTGCAAGCATGTTTAGAGGATAGTGTCTACACATAGAGATTAGGACATTTGTCT
 TGATTTGTGTGAGTCTTCTTGGGAATCATCTGCCCTCTCAGGCGGCTTTTGCAATAAAGTCTCTGAGGTGGGA
 TGTGCAAGGCTTAGGGGACATCTGGGGCTGTGAGAGCTACTGTGAGGAGGCTCACTPAGAAGCCCTTAATATTA
 GGAATTAAGGAACTATAAACTCAGTATGGGCTTAGGGATTTCTGTGACAGGAATATTTGCCCAATCACTAGTCT
 CTATCCATCTGTAGACACCAATTTCTCCATGCTCTGAGAAACCTGGGACATAGTTAGTAGGTAGTAATATCT
 GGAGCTCCTCGAGGAGCAAACTCCCAACTTTTCTTTCCCTCACTGACAGGCTGGAAATGATGCTTTGTATGTGG
 CAGATAGTAATTTTGGCATGCTTATATTTCTATCTGTAAAGTGTGACITTTATGAGACAGGCCCTTATAT
 ATGCATTTAAATTTGATATGGCAATATAACCCGAGGATCTGTAGATGAGGACCTGCTTTTCTTTCTCTC
 ATTGTCCCACTTACAAAGCTCAGTAGAATCTTCACTPCATACTCTCTCCAAAGGACGCTCAGAGAATTAG
 AACCGACCTTCTAACCAATTCACCCGCCACACCCCTCTACTGCTACTTTAAAAAAATTAATAGTTT
 CTATGAACCTGATCTAAGATGAAAAAATTAATTTCTTAATTTCTATAGCACTTTTATTTACATGACCTA
 AGACTATAAGAAATCTGATGGCAGTGAACAAGTGTAGCATTTATTTGTTATCTATAAAGACTTGTAGGACATA
 TGTGCAACTTATGAGTGTATCATGTTGTTCATGTAATTTTGGCCTTTTGTAAAGCTGGAACCTGTGAAGAAAT
 GAAAAATTAATTTTCTTTCTAGGACGACGATGAAAAAGCTATGAGATCTATGTTATCATCTGACGTAGT
 TGAACCACTTGCTGGTGTATGATGTGCTCTGTCTGTTTGAATGATTCATCTACTGCTCTTGTCTATT
 TCCCTTTGATGTTCAAGTCTGATCTATAGGATGGCGATTTAAAGCTTTACTCCCCCTTTAAATATAATGAT
 TBAAGTCTGCTCTTGA AAAA AAAAAA AAAAAA AAAAAA AAAAAA

FIGURE 38

MRPGLSFLLALLFFLQQAAGDLGDVGPPIPSPGFSSFPGVDSSSSSFSSSSSRSGSSSSSRSLGS
GGSVSQLFSNFTGSVDDRGTQCQSVSLPDTTFPVDRVERLEFTAHVLSQKFEKELSKVREYV
QLISVYEKKLLNLTVRIDIMEKDTISYTELDFELIKVEVKEMEKLVQLKESFGGSSEIVDQ
LEVEIRNMTLLVEKLETLDKNNVLAIRREIVALKTKLKECEASKDQNTPVVHPPPTPGSCGH
GGVNVNISKPSVVQLNWRGFSYLYGAWGRDYSPQHNPNGLYWVAPLNTDGRLLLEYRLYNTLD
DLLLYINARELRITYGQSGTAVYNNNMVYVNTGNIARVNLTTNTIAVTQTLPNAAAYNNR
FSYANVAWQDIDFAVDENGLWVIYSTEASTGNMVISKLNDTTLQVLNTWYTKQYKPSASNAF
MVCGVLYATRTMNTREEIFYYYDTNTGKEGKLDIVMHKMQEKVQSINYNPFQKLYVYNDG
YLLNYDLSVLQKPQ

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FIGURE 39

GCTCTGAAGACCAAGCTGAAAGAGTGTGAGGCCTCTAAAGATCAAACACCCCTGTCGTCCAC
CCTCCTCCCACTCCAGGGAGCTGTGGTCATGGTGGTGGTGAACATCAGCAAACCGTCTGT
GGTTCAGCTCAACTGGAGAGGGTTTCTTATCTATATGGTGCTTGGGGTAGGGATTACTCTC
CCCAGCATCAAACAAAGGNATGTATTGGGNGGCGCCATTGAATACAGATGGGAGACTGTTG
GAGTATTATAGACTGTACAACCCACTGGATGATTTGCTATTGTATATAAATGCTCGAGAGTT
GCGGATCACCTATGGCCAAGGTAGTGGTACAGCAGTTTACAACAACAACATGTACGTCAACA
TGTACAACACCGGGNATATTGCCAGAGTTAACCTGACC

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FIGURE 40

TCTCGCAGATAGTAAATAATCTCGGAAAGGCGAGAAAGAAGCTGTCTCCATCTTGCTGTGAT
 CCGCTGCCTCTTGACGCTTGGGAGATGGGGAGCGCTCTGGGGCTGTGCTCCATGGCGAGCT
 GGATACCATTTGTGTGGAAAGTGCCTCGTGTGGTATGCCGATGCTGCTAGTGGAAAC
 AACTCCACTGTAACATAGATTGATCTATGCACTTTCTTGCTGTGGAGATGTGTAGCTTG
 TGTAAATGTTGATACCGGAATGGAGAAACACTGAATAAGATTCTGGATTTGTGAGAAATC
 AGAAAGGTGTGTGCCCTTGAACATTTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTT
 GCTTTGGCTATGCTCTATCTCTCTCTCTTCTTCTAATGATCAAGGTGAAGGATAGCAGTGA
 TCCTAGAGCTGCAGTGCACAAATGGATTTGGTTCTTAAATTTGCTGGAGCAATTGCAATTA
 TTATTGGGCGATTCTCATCCAGAAGGAACCTTTACAACCTGTGGTTTTATGTAGGCATG
 CGAGTGGCTTTCTTTTCATCTCATACAACTAGTCTTACTTATGATTTTGCACATTCATG
 GAATGAATCGTGGGTTGAAAAATGGAAGAAGGGAACCTCAGATGTCTGATGCAAGCTTGT
 TATCACTACAGCTCTGAATATATCTGCTGTCTTTAGTTGCTATCGTCTGTGCTTTTGTCTAC
 TACACTCATCCAGCGATTGTTCAGAAAACAGGCGTTCATCATGTGCAACATGCTCCTCTG
 CGTTTGGTGTCTCTGTAATGCTATATACTGCCAAAAATCCAAGATCACACCAAGATCTGTT
 TGTTTACAGTCTTCAGTAATTACAGTCTACACAATGTATTTGACATGGTCAGCTATGACCAAT
 GAACCAAGAAACAAATGCACCCCAAGTCTACTAAGCATAAATGGCTACAATACAACCAAGAC
 TGTCCCAAAGGAGGGCAGTCAGTCCAGTGGTGGCATGCTCAAGGAAATATAGGACTTAATTC
 TCTTTTGTGTGTATTTTATTCAGCATCCGTACTTCAACCAATAGTCAGGCTTAATATAA
 CTGACTCTAACAAGTGATGATCTACATTAATAGAAGATGGTGGAGTAGAAGTGATGGATC
 ACTGGAGGATGGGAGCATGTTTACCAGCTGTAGATTAAGAAAGGGTGGTGTCTACTACA
 GTTATTCCTTCTTCACTTCATGCTTTTCCCTGGCTTCACTTATATCATGATGACCTTACC
 AACTGGTCCAGGTATGAACCTCTCGTGAGATGAAAGTCAAGTGAACAGCTCTGGGTGAA
 AATCTCTTCCGATTTGGATTGGCATCGTGTGTATGTTTGGACACTCGTGGCCTCACTTGTTC
 TTACAATCGTGATTTTGCATGAGTGTCTAGCATGAAAGTCCCACCTTTGATTTATTCG
 TTATTTGAAAACGATTTCCAACCTTTTGAAGTTGTGTATGTTTTTGTCTCCCATGTAAAC
 TTCTCCAGTGTCTGGAGATTAAGATTTTACTGCTGTGCTATTTGTTATTTCTTACCAA
 GTGCATTGATATGTGAAGTAGAATGAATTCAGAGGAAAGTTTATGAATATGGTGATGAGT
 TAGTAAAAGTGGCCATTATTTGGGCTTATTTCTCTGCTCTATAGTTGTGAATGAAGATAAAA
 ACAAAATTTGTTTGACTATTTTAAAATATATTAGACCTTAAGCTGTTTGTAGCAAGCATTAAA
 GCAAAATGTATGGCTGCCTTTTGAATATTTGATGTGTTTGCCTGGCAGGATACCTGCAAGAAC
 ATGGTTTATTTTAAAAATTTATAAACAAGTCACTTAATGCCAGTTGTCTGAAAATCTTATA
 AGGTTTACCCTTGATACGGAATTTACACAGGTAGGAGTGTATTAGTGACATAGTGTAGG
 TTATGGATGGAGGTGTCGGTACTAAATGAATAACAGAGTAAATCTTACTTGGGTAGTAC
 TGGCCTTTGCCAACAAAGTGAACCTGTTTGGTGTGTTTAAACTCATGAAGTATGGGTTCAGT
 GGAAATGTTTGAACACTGAAGGATTTAGACAAGGTTTGAAGAGGATAATCATGGGTACAG
 AGGAAGTGTTTGAAAGTCACTTTGAAAGTTAGTATTTGGGCCCCAGCACGGTAGCTCACCTT
 GGTAATCCAGCACTTTGGGAGCTTAAGTGGGTAGATTACTTGAGCCAGGAATTCAGACCA
 GCTTGGCAGATGGTGAACCTGTCTTATAAAAAATTAATCTGGCTTTGAGCATATGCCTGTGGTC
 CAGCATGAGAGGCTAGTGAAGATTGCTGAGCCAGAGCCAAAGGTTGCAGTAGGCAAGTCA
 CGTCACTGCACCTAGCTTGGCAGAGAGTAAGCCAAAAAATATATATATTTGAAATCAAGG
 AGCCAAAATTTTGAAGGGAAGTAAGTAACTGCAAAACCCTAGGCTTTAGTAGGTACTTAT
 ATAAAACTAGTCCAGTTCTCTCATTTAAAAAATGAAGACACTGAAATACAGACTTAAATA
 GCTCAGATAGCTAAATTAGGAATTTCAAGTTGGCCAATAATAGCATCTCTCTGACATTTAA
 AAATAAATTTCTATTTCAAATACATGCATATTGATTTACACCTCATACTGTGATAAATTAAGT
 GATGTGGATTGCTGGTGTCCAGCATGAACCAATAACAGGTCAGAAAGATGATGAATGTTT
 AGAATAAACTCCTGCTTATAGTATACTACACAGTTCAAAGATGTTTAAATGCTTTTGTAT
 TTACTGCCATGTAATGAAATATATAGATTATGTAACTTTCAACCTGAAATCAAGCAT
 ATGAGAGTTTAGTTATTTGTATGTGTCACTAGTGTCTAATGAAGCTTTTAAATCTCAAAAT
 TCTTCTTTAAAAATATTTAATGTGAATGGAATATAACAATCAGCTTAATTTCCCAACC
 TTATTTCTGTGTGTAGACATTGTATCCACAATTTTGAATGGCTGTGTTTACCTCTAAATAA
 ATGAATTCAGAGAAAAA

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MGSVLGLCSMASWIPCLCGSAPCLLRCCPCSGNNSTVTRLIYALFLLVGVCVACVMLIPGME
 EQLNKIPGFCENEKGVPCNINLVGYKAVYRLCFLGLAMPYLLLSLLMIKVKSSSDPRAAVHNG
 FWFFKFAAAIAIIIGAFPIPETFTTVWFVVGMAGAFCPILIQVLVIDFAHSWNESWVEKM
 EEGNSRCWYAALLSATALNYLLSLVAIVLFFVYTHPASCSENKAFISVNMLLCVGASVMSI
 LPKIQESQPRSGLLQSSVITVYTMYLTSAMTNEPETNCNPSSLIIIGYNTTSTVPKEGQSV
 QWWHAQGIIGLILFLLCVFYSSIRTSNNSQVKNLTLSDESTLIEDGGARSDGSLEDGDDVH
 RAVDNERDGVTVYSYFFHFMLFLASLYIMMTLTNWSRYEPSREMKSWQTA VVVKISSWIGI
 VLYVWTLVAPLVLTRNDFD

GCGAGAAAGAAGCTGCTCCATCTTGTCTGTATCCCGCTGCTTCTTNGACGTTGTGGAGAT
GGGGAGCGTCCCTGGGGCTGTGCTCCATGGCGAGCTGGATAACATGTTTGTGTGGAAGTGCC
CCGTTGTTTCTATGCCGATGCGTCTCTAGTGGAACAANTCCACTGTAACATGATGATCTA
TGCACTTTTCTTGCTTGTGGAGTATGTGTAGCTTGTGTAATGTTGATACCGGAATGGAAG
AACAACTGAATAAGATTCTGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAACATT
TTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTGTGGTTTGGCTATGCTCTATCTTCTCT
CTGTTTACTAATGACAAGGTAGAGTAGCAGTAGCTTACGCTTAGCTGCAGTGCACAATGGAT
TTTGTTCTTTTAAATTTGCTGCAGCAATTGCAATTTATTTATTTGGGGC

FIGURE 43

GTTATTGTGAACCTTTGTGGAGATGGGAGGTCNTGGGGCTGTGTTCCATGGCGAGCTGGATAC
CANGTTTGTGTGGAAGTGCCCGTGTGTTGNTATGCCGATGCTGTCCTAGTGGAACAANTCC
ACTGTAATTAGATTGATNTATGCACTTTTNTTGCTTGTGAGTANGTGTAGCTTGTGTAAT
GTTGATACCAGGAATGGAAGAACAACGAATAAGATTCTCGGATTTTGTGAGAATGAGAAAG
GTGTTGTCCCTTGTAACATTTGGTTGGCTATAAAGCTGTATATNGTTTGTGCTTTGGTTTG
GCTANGTTCTATNTTCTTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAG
AGCTGCAGTGCACAATGGATTTTGGTTTTTAAATTTGCTGCAGCAATTGCAATTATTATTG
GGGC

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FIGURE 44

AAGAAGCTGTCTCCATCTTGTCTGTATCCGCTGCTCTTGTGAACGTTNTGGAGATGGGGAGC
GTCCITGGGGTTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCCCGTGTT
TGCTATGCCGATGCTGTCTAGTGGAACAACCTCCACTGTAACTAGATTGATCTATGCACTT
TTCTTGCTTGTGTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAGAACAAC
GAATAAGATTCTTGGAATTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAAACATTTTGTTG
GCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTCTCTTTTA
CTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTGTT
CTTTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGC

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FIGURE 45

GCTGTCCTTAGTGGAACAANTCCAACCTTGTAACCTGGATTGATCTATGCACCTTTTCCTTG
CTTGTTGGAGTATGTGTAGCTTTGTGTAATGTTGTTCCAGGATTGGANGAACAACTGAATA
AGATTCTCGGATTTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAACATTTTTGGTTGGC
TATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTTCTCTTTACT
AATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTGGTTCT
TTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGCATTCTTCATTCCAGAAGGAACCTTT
ACAACTGTGTGGTTTTATGTAGGCATGGCAGGTGCCTTTTGTTCATCCTCATACAACCTAGT
CTTACTTATTGATTTTGCACATTGATGGAATGAATCGTGGGTGAAAAAATGGAAGAAGGGA
ACTCGAGATGTTGGTATGCAGCCTTGTTATCAGCTACAGCTCTGAATTATCTGCTGTCTTTA
GTTGCTATCGTCTCTGTTCTTTGCTCTACTACACTCATCCAGCCAGTTGTTTCAGAAAACAAGGC
GTTTCATCAGTGTCACATGCTCCTCTGCGTTGGTGCTTCTGTAATG

FIGURE 46

CTCGGCGCGCACAGGCAGCTCGGTTTGGCCCTGCGATTGAGCTGCGGGTTCGGGCGCGGCGCGGCGCTCTCCAAT
GGCAATGTGTGTGCTGGAGGGGAGCGCAGGCTTCGGCAAAGGCAGTGCAGTGTTCGACACCGGGGGCGAG
TCCTGTGAAGCAGATAGAAAGAAACATTTATTACCTGTCTATTACGAGGAGCGCCGCGCGGCTGCTCGC
ACTCCCGCGGAACATTTGGCTCCCTCCAGCTCCGAGAGAGGAGAGAAAGAAAGCGGAAAGAGCAGATTTAC
GTGCTTTCAGCCCAAGTGGACCTGATCGATGGCCCTCTGAATTTATCACGATATTTGATTTATTCAGCATGCC
CCCTGGTTTGTGTGTACGCACACACAGCTGCACACAAGGCTCTGGCTCGCTCCCTCCCTCGTTTCAGCTCTC
TGCGCGAATCCCACTATCTGTTTCAACTCTCCGCGAGGGCGAGGAGGCGAGAGTGTGTGCAATCTCGGAGTG
AAGAGGACGAGGGGAAAAAAGCAAGGCCACAGACGCACTTGAGACTCCCGCATCCCAAGAAAGCACACAGAT
CAGCAAAAAAGAAAGATGGGCCCCCGAGGCTCTGTGCTGTGCTGTGCTCCGCAACTGTGTTCCCTCGTGGG
TGGAGCTCGGCTCTCTGTGCGACCCCGCTGAAAGGCAGGTTTCAGAGGGACCGAGGAACATCCGCGCCA
ACATCATCTCTGTGCTGACGGAGCAGCAGGATGTGGAGCTGGGTTCCATGCAAGGTGATGAACAAGACCCGCGC
ATCATGGAGCAGGGCGGGGCGCACTTTCATCAACGCTCTGTCACCAACACCTACACCAACATGAGAATGCTCTCGCCCTCTCTGCG
AGGCACAGCACGAGAGCGCACCTTTGCGCTGTACTCTCAATGACTGGCTACCGGACAGGCTTTCTTCGGGAAG
TATCTTAATGAATACACCGCTCTTACGTGCCACCCGCTTGGAGGAGTGGGTGGGACTCTTAAAAATCCCG
CTTTTATAACTACAGCTGTGTGCGAACGGGTGAAGAGAGACGCGCTCCGACTACTCCAAGGATTACCTCA
CAGGCTCATCAACCAATGACAGCTGTGAGCTTCTTCGCGAGCTCCAAGAAAGTGTACCCGACAGGCGAGTCTCT
ATGGTCTTCAGCATGACAGCCCCCGCCCTGAGGATTACGCCCCCACTATTCAGCGCTCTCTCCCAAGCG
ATCTCAGCACAATCAGCGGAGCTACAACATACGCGCCCAACCCGGAACAACTGGATCATGGCTACACGGGGG
CCATCAGGCCCATCCACATGGAATTCACCAACATGCTCCAGCGGAAGCGCTTGCAGACCTCATGTCGGTGGAC
GACTCCATGGAGACGATTTACAACATGTGGTTGAGACGGGCGAGCTGGACAACAGTACATCGTATACACCGG
CGACCAGGTTTACCACCTGCGGCAGCTTTGGCGCTGGTGAAGGGAAATCCATGCCATATGAGTTGACATCAGGG
TCCGCTTCTACGTGGAGGGGCCCCAAGTGGAGCGCGCTGTGTAATCCCACTCATGCTCTCAACATGACCTG
GCCCCACCACTCTGGACATCTGAGGCTTGGACATACCTGCGGAGTGGAGCGGAAATCCATCTCAAGCTGTG
GGACAGCGAGCGCGCGTGAATCGGTTTCACTTGAAGAAAGATGAGGCTGAGGCGGACTCTCTTGTGGTG
AGAGGCGCAAGCTGTACACAAGAGACANTGACAGGTGGAGCGCCAGCGGACGATTTCTGCGCAAGTAC
CAGGCTGTGAAGGACTGTGTGAGCTGTGATACGACGCGGCTGTGAGCAGCTGGGACAGAGTGGCAGTG
TGTGAGGAGCGCCACAGGGGAAGCTGAAGCTGCATAAGTGCAGGGGCCATCGGCTGGGCGGACAGAGGCC
TCTCCAACTCTGTCGCCAAGTACTACGGGACGGCAGCGAGGCTGCACCTGTGACAGCGGGGACTACAAGCT
AGCCTGGCCGCGCCACAGGGGAAGCTTCAAGAAAGTACAAAGGCCAGCTATGTCCGAGCTCGCTCCATCG
CTCAGTGGCCACTCAGGTGGAGCGCAGGGTGTACCACTAGCGCTGGGTGATCGCGCCAGCGCCGAAACCTCA
CCAAGCGCACTGGCAGGGGCCCCGAGGACCAAGATGACAAGATGGTGGGACTCTCAGTGGCATGGAGG
CTTCCGCACTACTCAGCGGCCAACCCCATTAAGTGCACATCGGTGCTACCTAGAGAACGACAGCTCA
TGTGTGACCTGGACCTGTACAGTCCCTGCGAGGCTGGAAGACCAAGCTGCACATGCACACAGAGATTGAAA
CCCTGCAGAACAAATTAAGAACTGAGGGAAGTCCGAGGTCACCTGAAGAAAAAGCGGCGCAGAAGATGTGAC
TGTCACAAAATCAGCTACCAACCCGACGACAAAGGCCGCTCAAGCACAGAGGCTCAGTCTGCATCTTTTCA
GAAGGCGCTCAAGAGAAAGGACAGGTGTGGCTGTGCGGGAGCAGAAGCGCAAGAGAAACTCGCAAGCTGC
TCAAGCGCTCTGCAACACAGACAGCTGTGAGCATGCCAGGCTCAGTGCTTACCCACGACAAACAGCAGCTGG
CAGACGGCGCTTTCTGGCACTGGGGCTTTCTGTGCTGCACCGAGCCCAACATACACGTAAGTGTGAT
GAGGACCATCAATGAGACTCACATTTCTCTTCTGTGAATTTGCAACTGGCTTCTAGAGTACTTTGATCTCA
ACACAGACCCCTCCAGCTGATGAATGAGTGAACACATGGACAGGATGTCTCTCAACAGCTACAGCTACAG
CTCATGTGAGCTGAGGAGCTGCAAGGGTTTACAAGCAGTGTAAACCCCGGACTCGAACAACATGGACCTGGATGGAG
AAGCTGTGACCAATACAGGCACTTTCAAGCTGCAAGTGGCCAGAAATGAAGAGACTTTTCAAACTCATGG
GACAATGTGGGAAGGCTGGGAAGTTTAAAGAAACACAGAGTGCACCTCCAAAAACATAGAGGCATCACTGA
CTGCAGGCAAGTGAAGAACTGTGGGTGATTTCAGCAGGAGCTGTGCTATTGGCCAGAGGCTCTGAGAAGC
AAGCAGCCTCTCAGTCAACATGACAGATTCTGGAGGATAACAGCAGGAGCAGAGATACTCTCAGGAAGTCC
ATTTTTGCCCCCTGTTTGGTTTGGATTATACCTCACCAGCTGCACAAATGCTATTTTTCTGATCAAAAGT
ACCACATACCTCCCCAGAGACTCAAAAGGAAAGCGAGAGAGCGAGGAGAGATTTCTTGGAAATTTCT
TCCCAAGGGCGAAAGTCAATTGGAATTTTAAATCATAGGGGAAAGCAGTCTGTCTTAAATCCTTATTCTT
TTGGTTTGTCAAAAGAGGAATTAAGAGCAGGACAGAGGCAAGCTGGAGAGGCTGAAGAACGTGAGAGAGC
TTTGAAATGAGTCACTAGTACACAAAGAGATGACATTTTACCTAGCATAAACCCTGGTTGCCCTGAAGAAA
CTGCCCTTCAATGTATATATGTGACTATTACATGTAATCAACATGGGAACCTTTTAGGGGAACCTAATAGAAAT
CCCAATTTTCAGGAGTGGTGGTCTCAATAAACGCTCTGTGCCAGTGTAAAAAGAAA

FIGURE 47

MGPPSLVLCLLSATVFSLLGGSSAFLSHHRLKGRFQRDRRNIRPNIIILVLTDDQDVELGSMQ
 VMNKTRRIMEQGGAHFINAFVTTMCCPSRSSILTGKYVHNHNTYTNNENCSSPSWQAQHE
 RTFAVYLNSTGYRTAFFGKYLNEYNGSYVPPGWKEWGGLLKNSRFYNYTLCRNGVKEKHGSD
 YSKDYLTDLITNDSVSFFRTSKKMYPHRPVLMVISHAAPHGPEDSAPQYSRLFPNASQHITP
 SYNYAPNPKHWIMRYTGPMKPIHMEFTNMLQRKRLQTILMSVDDSMETIYNMLVETGELDNT
 YIVYTADHGYHIGQFGLVKGKSMPIYEFDIRVPFYVRGPNVEAGCLNPHIVLNIDLAPTILDI
 AGLDIPADMDGKSILKLLDTERFPVNRFHLLKKMRVWRDSFLVERGKLLHKRDNDKVDAQEEN
 FLPKYQVRVKDLCQRAEYQTACEQLGQKWQCVEDATGKLKLHKCKGPMRLGGSRALSNLVPKY
 YGQGEACTCDSGDYKLSLAGRRKKLFKKKYKASYVRSRSIRSVAIEVDGRVYHVGLGDAQ
 PRNLTKRHWPAPEDQDDKDGDFSGTGGLPDYSAANPIKVTHRCYILENDTVQCDDL DLYKS
 LQAWKDKHLHIDHEIETLQNKIKNLREVRGHLKKKRPEECDCHKISYHTQHKGRLKHRGSSL
 HPFRKGLQEKDKVLLREQKRKKLRKLLKRLQNNDTCSMPGLTCFTHDNQHWQTAPFWTLG
 PFCACTSANNNTYWC MRTINETHNLFCEFATGFLEYFDLNTDPYQLMNAVNTLDRDVLNQL
 HVQLMELRSCKGKYQCNPRTNRNMDLDGGSYEQYRQFQRRKWPEMKRPSSKSLGQLWEGWEG

FIGURE 48

AACAAAGTTCAGTGACTGAGAGGGCTGAGCGGAGGCTGCTGAAGGGGAGAAAGGAGTGAGGA
 GCTGCTGGGCAGAGAGGGACTGTCCGGCTCCAGATGCTGGGCCTCCTGGGGAGCACAGCCC
 TCGTGGGATGGATCACAGGTGCTGCTGTGGCGGTCTGCTGCTGCTGCTGCTGCTGGCCACC
 TGCCTTTTCCACGGACGGCAGGACTGTGACGTGGAGAGGAACCGTACAGCTGCAGGGGGAAA
 CCGAGTCCGCCGGGCCAGCCTTGGCCCTTCCGGCGGCGGGGCCACCTGGGAATCTTTCACC
 ATCACCGTCATCCTGGCCACGTATCTCATGTGCCGAATGTGGGCCTCCACCACCACCACCAC
 CCCCGCACACCCCTCACCACTCCACCACCACCACCACCCCCACCGCCACCATCCCGCCA
 CGCTCGCTGAGGCTGCTGTCGCCGTGCCTGTGGACAGCAGCTGCCCTGCCCTCCCATCTG
 TTCCCAGGACAAGTGGACCCCATGTTCCATGTGGAAGGATGCATCTCTGGGGTGAACGAGG
 GGAACAATAGACTGGGGCTTGCTCCAGCTGCATTTGCATGGCATGCCCCAGTGTACTATGGC
 AGCAGAGAATGGAGGAACACTGGGTCTGCAGTGCTGAAGGGTTTGGGGAGTGGAGAGCAAGG
 GTGCTCTTTCGGGGCTGGACAGCCCGTCTTGTGACAGTGACTCCAGTGAGCCCAGAAATG
 ACAAGCGTGCTTGGCAGAGCCAGCACACAAGTGGATGTGAAGTGCCCGTCTTGACCTCCTC
 ATCAGGCTGCTGCAGGCCTCTGGCGGGCAGGGCACTGGGAGAGGCCCTGAGAATGTCTTTT
 GGT TTGGAGAAGGCAGTGTGAGGCTGCACAGTCAATT CATCGGTGCCTTAGTCCAAGAAAAT
 AAAAACCCTAAGAAGCTTTAAAAAAAAAAAAAAAAAAAAA

FIGURE 49

MLGLLGSTALVGWITGA AVAVLLLLLLLATCLFHGRQDCDVERNRTAAGGNVRRAPWPFR
RRGHLGIFHHHRHPGHVSHVPNVGLHHHHHPRHTPHHLHHHHHPHRRHPRHAR

GGCGGCTGCTGAGCTGCCCTTGAGGTGCAGTGTGGGGATCCAGAGCC**CATG**TCGGACCTGCTA
CTACTGGGCTGATTGGGGGCTGACTCTCTTACTGCTGCTGACGCTGCTGGCCTTTGCGCG
GTACTCAGGGCTACTGGCTGGGGTGAAGTGAGTGCTGGGTACCCCCCATCCGCAACGTCA
CTGTGGCCTACAAGTTCCACATGGGGCTCTATGGTGAGACTGGCGGCTTTTCACTGAGAGC
TGCAGCATCTCTCCCAAGCTCCGCTCCATCGCTGTCTACTATGACAACCCCCACATGGTGCC
CCCTGATAAAGTGCCGATGTGCCGTGGGCAGCATCCTGAGTGAAGGTGAGGAATCGCCCTCCC
CTGAGCTCATCGACCTCTACCAGAAATTTGGCTTCAAGGTGTTCTCCTTCCCGGCACCCAGC
CATGTGGTGACAGCCACCTTCCCCTACACCACCATTCTGTCCATCTGGCTGGCTACCCGCCG
TGTCATCTCGCTTGGACACCTACATCAAGGAGCGGAAGCTGTGTGCCTATCCTCGGCTGG
AGATCTACCAGGAAGACAGCATCTTTCATGTGCCCCACTGGCAGCGGAGGAGACTTCTAT
GTGCCGTGAGATGAAGGAGACAGAGTGGAAATGGCGGGGGCTGTGTGAGGCCATTGACACCCA
GGTGGATGGCACAGGAGCTGACACAATGAGTGACACGAGTTCTGTAAGCTTGAAGTGAGCC
CTGGCAGCCGGGAGACTTCAGCTGCCACACTGTCACTGGGGCGAGCAGCCGTGGCTGGGAT
GACGGTGACACCCGACGCGAGCACAGCTACAGCGAGTCAGGTGCCAGCGGCTCCTCTTTTGA
GGAGCTGGACTTGGAGGGCGAGGGGCCCTTAGGGGAGTACGGCTGGACCTGGGACTGAGC
CCCTGGGGACTACCAAGTGGCTCTGGGAGCCACTGCCCTTGAGAAGGGCAAGGAG**TAA**CCC
ATGGCCTGCACCTCCTGCACTGCAGTTGCTGAGGAAGTGCAGACTCTCCAGCAGACTCT
CCAGCCCTCTTCTCCTTCTCTGTTGGGGAGGAGGGGTTCCTGAGGGACCTGACTTCCCTTGC
TCCAGGCCTCTTGCTAAGCCTTCTCCTCACTGCCCTTAGGCTCCAGGGCCAGAGGAGCCA
GGGACTATTTTCTGCACCAGCCCCAGGGCTGCCGCCCTGTTGTGTCTTTTTTCAGACTC
ACAGTGGAGCTTCCAGGACCCAGAATAAGGCCAATGATTACTTGTTCACCTGGAAAAAAA
AAAAA

FIGURE 51

MSDLLLLGLIGGLTLLLLLTLLAFAGYSGLLAGVEVSAGSPPIRNVTVAYKFHMGLYGETGR
LFTESCSISPKLRSIAVYYDNPHMVPPDKCRCVAGSILSEGEESPSPELIDLYQKFGFKVFS
FPAPSHVVTATFPYTTILSIWLATRRVHPALDTYIKERKLCAYPRLEIYQEDQIHMCPLAR
QGDFYVPEMKETEWKRWGLVEAIDTQVDGTGADTMSDTSSVSLEVSPGSRETSAAATLSPGAS
SRGWDDGDTRSEHSYSSESGASGSSFEELDLEGEGPLGESRLDPGTEPLGTTKWLWEPTAPEK
GKE

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FIGURE 52

CCGCGGGAACGCTGTCTGGCTGCCGCCACCCGAACAGCCTGTCTTGGTGCCCCGGCTCCCT
 GCCCGCGCCAGTC**ATG**ACCCTGCGCCCTCACTCCTCCGCTCCATCTGCTGCTGCTGCT
 GCTGCTCAGTGCGGCGGTGTGCCGGCTGAGGCTGGGCTCGAAACC GAAAGTCCCGTCCGGA
 CCTCCAAGTGGAGACCCTGGTGGAGCCCCAGAACCATGTGCCGAGCCGCTGCTTTTGA
 GACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCT
 GACCAGAGACCCTCTGGTTATAGAAGTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGA
 GTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCTTCTCACTTGGCCTAT
 GGAAAACGGGGATTTCACCATCTGTCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCT
 GATTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGGGCATTTTGCCTCTGGTAG
 GGATGGCCATGGTGCCAGCCCTCCTGGGCTCATTTGGGTATCACCTATACAGAAAGGCCAAT
 AGACCCAAAGTCTCCAAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAA**TA**
ATAAATAATAAATTTAAAAAACTTAAAAAAAAAAAAAAAAAAAA

FIGURE 53

MTLRPSLLPLHLLLLLLLLSAAVCRAEAGLETESPVRTLQVETLVEPPEPCAEPAAFGDTLHI
HYTGSLVDGRIIDTSLTRDPLVIELGQKQVIPGLEQSLDMCVGEKRRAIIPSHLAYGKRGF
PPSVPADAVVQYDVELIALIRANYWLKLVKGILPLVGMAMVPALLGLIGYHLYRKANRPKVS
KKKLKEEKRNKSKKK

FIGURE 54

CCCGGGAACGTGTTCTCTGGCTGCCGCACCCGAACAGCCTGTCTGGTGCCCGGGCTCCCTGC
 CCCGCGCCAGTCATGACCCTGCGCCCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCTGC
 TGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAAGTCCCGTCCGGACC
 CTCCAAGTGGAGACCCCTGGTGGAGCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGGAGA
 CACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCTGA
 CCAGAGACCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGAGT
 CTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCTTCTCACTTGGCCTATGG
 AAAACGGGGATTTCACCATCTGTCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCTGA
 TTGACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGGGCATTCTTGCCTCTGGTAGGG
 ATGGCCATGGTGCCACCCTCCTGGGCCTCATTGGGTATCACCTATACAGAAAGGCCAATAGA
 CCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAAATAATA
 AATAATAAATTTAAAAAACTTA

FIGURE 55

CCGAAAGTCCCGTCCGGACCCCTCCAAGTGGAGACCCTGGTGGAGCCCCCAGAACCATGTGCC
GAGCCCGCTGCTTTTGGAGACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACG
TATTATTGACACCTCCCTGACCAGAGACCCTCTGGTTATAGAAGCTTGGCCAAAAGCAGGTGA
TTCCAGGTCTGGAGCAGAGTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATT
CCTTCTCACTTGGCCTATGGAAAACGGGGATTTCCACCATCTGTCCCAGCGGATGCAGTGGT
GCAGTATGACGTGGAGCTGATTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGG
GCATTTTGCCTCTGGTAGGGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATCAC
CTATACAGAAAGGCCAATAGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAA
CAAGAGCAAAAAGAAATAATAAATAATAAATTTAAAAAACTTAAAA

FIGURE 56

CTGCTGCATCCGGGTGTCTGGAGGCTGTGGCCGTTTTGTTTTCTTGGCTAAAAATCGGGGGAG
 TGAGGCGGGCCGGCGCGCGACCCGGGCTCCGGAACCACTGCACGACGGGGCTGGACTG
 ACCTGAAAAAAATGTCTGGATTTCTAGAGGCTTGAGATGCTCAGAATGCATTGACTGGGGG
 GAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTACTATTTTTTACAGGCTGGTGGAT
 TATCATAGATGCAGCTGTTATTTATCCACCATGAAAGATTTCAACCACTCATACCATGCCT
 GTGGTGTATATAGCAACCATAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGA
 GGTGATAGTTACAGTGAAGTTGTCTGGGTCAAACAGGTGCTCGCATTTGGCTTTTCGTTGG
 TTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTATGTGTG
 CTAAAGAAAAAGACATAGTATACCCTGGAATTGCTGTATTTTTCCAGAATGCCTTCATCTTT
 TTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGACTTATGGCAGTGAACACATCTGAT
 TTCCACAGCACAAACAGCCCTGCATGGGTGTGTTGTTTTTACTGCTCACTCCCAACCTT
 TTGTAATGCCATTTCTAAACTTATTTCTGAGTGTAGTCTCAGCTTAAAGTTGTGTAATACT
 AAAATCACGAGAACCCTAAACAACAACCAAAAATCTATTGTGGTATGCACTTGATTAACCT
 ATAAAAATGTTAGAGGAACTTTACATGAATAATTTTGTCAAATTTTATCATGGGTATAATT
 TGTAATAATAAAGAAATTACAAAAGAAATTATGGATTTGTCAATGTAAGTATTTGTCATA
 TCTGAGGTCCAAAACCAATGAAAGTGCTCTGAAGATTTAATGTGTTTATTCAAATGTGGT
 CTCTTCTGTGTCAAATGTTAAATGAAATATAAACATTTTTTAGTTTTTAAATATTCCGTGG
 TCAAAATCTTCTCACATATAATTGGTATTTACTTTTACCAAAAATCTGTGAACATGTAAT
 GTAACCTGGCTTTTGAGGGTCTCCCAAGGGGTGAGTGGACGTGTTGGAAGAGAGAAGCACCAT
 GGTCCAGCCACCAGCTCCCTGTGTCCTTCCATGGGAAGGTCTTCCGCTGTGCCTCTCAT
 CCAAGGGCAGGAAGATGTGACTCAGCCATGACACGTGGTCTGGTGGGATGCACAGTCACTC
 CACATCCACCCTG

FIGURE 57

MSGFLEGLRCSECIDWGEKRNTIASIAAGVLFFTGWWIIIDA AVIYPTMKDFNHSYHACGVI
ATIAFLMINAVSNGQVRGDSYSEGCLGQTGARIWLFVGFMLAFGSLIASMWILFGGYVAKEK
DIVYPGIAVFFQNAFIFFGGLVFKFGRTEDLWQ

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FIGURE 58

TTCTTGGCTAAAATCGGGGGAGTGAGGCGGGCCGGCGCGGACACCGGGCTCCGGAACC
ACTGCACGACGGGGCTGGACTGACCTGAAAAAATGTCTGGATTCTAGAGGGCTTGAGATG
CTCAGAATGCATTGACTGGGGGGAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGATC
TATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGTTATTTATCCCACCATGAAAGAT
TTCAACCACTCATAACCATGCCTGTGGTGTTATAGCAACCATAGCCTTCCTAATGATTAATGC
AGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTGCTGGGTCAAACAGGTG
CTCGCATTGGCCTTTTCGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGG
ATTCTTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTATACCCTGGAATTGCTGTATT
TTCCAGAATGCCTTCATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGC

FIGURE 59

TGGACGGACCTGAAAAAATGTTTGGATTNTAGAGGNTTGAGATGTTTCAGAATGCATGAC
TGGGGGAAAAGCGCAAATACTATTGCTTCCATTGCTGCTGGTGTANTATTTTTTACAGGCTG
GTGGATTATCATAGATGCAGNTGTTATTTATCCCACCATGAAAGATTTCAACCANTCATACC
ATGCCTGTGGTGTATAGCAACCATAGCCTTCNTAATGATTAATGCAGTATCGAATGGACAA
GTCCGAGGTGATAGTTACAGTGAAGGTTGTTTGGGTCAAACAGGTGCTCGCATTGGCTTTT
CGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTT
ATGTTGCTAAAGAAAAAGACATAGTATACCCTGGAATTGNTGTATTTTTCCAGAATGCCTTC
ATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGANTTATGGCAGTG

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FIGURE 60

GGACACCGGGTTCCGGACCAATGCANGACGGGGTGGANTGACCTGAAAAAATGTTTGGATT
TTTAGAGGGCTTGAGATGNTCAGAATGCATTGACTGGGGGAAAAGCGCAATANTATTGCTTT
CCATTGCTGCTGGTGTACTATTTTTTACAGGGTGGTGGATTATCATAGATGCAGCTGTTATT
TATCCCACCATGAAAGATTTNAACCACTCATACCATGCCTGTGGTGTATAGCAACCATAGC
CTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTT
GTTTGGGTCAAACAGGTGNTCGCATTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATTT
CTGATTGNATTCTATGCGGATTCTTCTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTAT
ACCCTGGAATTNCTNTATTTTTCCAGAATGCC

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104111.22406660

FIGURE 61

TAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGAAAAGCGCAATANTATTGCTTCC
ATTGNTGNTGGTGTANTATTTTTTTACAGGCTGGTGGATTATNATAGATGCAGCTGTTATTT
ATCCCACCATGAAAGATTTNAACCANTCATACCATGCCTGTGGTGTTATAGCAACCATAGCC
TTCCTAATGATTAATGCAGTATNGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTG
TTTGGGTCAAACAGGTGNTNGCATTGCGCTTTTNGTTGGTTTCATGTTGGCCTTTGGATCTN
TGATTGCATTTATGTGGATTNTTTTTGGAGGTTATGTTGCTAAAGNAAAAGACATAGTATAC
CCTGT

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GGGAGGCTGTGNCGGTITTTGTTTTNTTGGCTAAAATCGGGGGAGTGAGGCGGCCCGGCGCG
CGNGACACCGGGTTCCGGGAACCATTTGCACGACGGGGTGACTGACCTGAAAAAATGTTTG
GATTNTAGAGGGCTTGAGATGCTCAGAAATGCATTGACTGGGGGGAAAGCGCAATACTATT
GCTTCCATTGCTGCTGGTGTACTATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGT
TATTTATCCCACCATGAAAGATTTCAACCACTCATACCATGCCTGTGGTGTATAGCAACCA
TAGCCTTCCTAATGATTAATGCGATATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAA
GGTGTGCTGGGTCAAACAGGTGCTCGCATTTTGGCTTTTCGTTGGTTTCATGTTGGCCCTTTGG
ATNCTGATGTGCATCTATGTGGATCTTTTTGGAGGTTTATGTTGCTTAAGAAAAAGACATAG
TATACCCTGGAATTGCTGTATTTTTCCAGAATGCCTCATNTTTTTGGAGGGGCTG

FIGURE 63

CGACGCCGCCGCGT**GATG**TGGCTTCCGCTGGTGTCTCTGGCTGTGCTGCTGCTGGCCGTCC
TCTGCAAGATTTACTTGGGACTATTCTCTGGCAGCTCCCCGAATCCTTTCTCCGAAGATGTC
AAACGCCGCCCAGCGCCCTGGTAACTGACAAGGAGGCCAGGAAGAAGGTTCTCAAAACAAGC
TTTTTCAGCCCAACCAAGTGGCGCAGAGCTGGATGTGGTGGTAATTTGGCAGTGGCTTTGGGG
GGCTGGCTGCAGCTGCAATTTCTAGCTAAAAGCTGGCAAGCGAGTCTGGTGTGGAAACAACAT
ACCAAGCGACGGGGCTGCTGTCTACACTCTTTGGAAAGAAATGGCCCTGAAATTTGACACAGGAAT
CCATTACATTGGGCGTATGGAAGAGGGCAGCAATTGGCCGTTTATCTTGGACCGAGATCACTG
AAGGGCAGCTGGGACTGGGCTCCCTGTCTCTCTCTTTTACATCATGGTACTGGAAGGGCCC
AATGGCCGCAAGGAGTACCCCATGTACAGTGGAGAGAAAGCCTACATTCAGGGCCCTCAAGGA
GAAGTTTCCACAGGAGGAAGCTATCATTGACAACTATATAAAGCTGGTTAAGGTGGTATCCA
GTGGAGCCCCCTCATGCCATCTCTTTGAAATTTCTCCCATTCGCCCTGGTTCAGCTCTCTCGAC
AGGTGTGGGCTGCTGACTCGTTTCTCTCCATTCTTCAAGCATCCACCCAGAGCCTGGCTGA
GGTCTCTGCAGCAGCTGGGGGGCTCTCTGAGCTCCAGGCAGTACTCAGTACATCTTCCCCA
CTTACCGTGTGCACCCCAACACAGTGCCTTTTCAATGCAGGCCCTGCTGGTCAACCACTAC
ATGAAGAGGAGCTTTTATCCCGCAGGGGGTTCCAGTGAATTCCTTCCACACCATCCCTGT
GATTCAGCGGGCTGGGGCGCTGTCTCACAAAGGCCACTGTGCAGAGTGTGTTGTCTGGACT
CAGCTGGGAAGGCTGTGGTGTCTAGTGTGAAGAAGGGCATGAGCTGGTGAACATCTATTGG
CCCATCGTGTCTTCCAAAGCAGGACTGTTCAACACCTATGAACACCTACTGCCGGGGGAAGCC
CCGCTGCTCCAGTGTGAAGCAGCAACTGGGGACGGTGGGGCCGGCTTAGGCATGACCT
CTGTTTTCTATCTGCTGCGAGGCACCAAGGAAGACCTGCATCTGCCCTGCCACCACTACTAT
GTTTACTATGACACGGACATGGAACAGGCGATGGAGCGCTACGCTCCATGGCCAGGGAAGA
GGCTGGCGGAACACATCCCCCTTCTCTTCTTCGCTTTCCCATCAGCCAAAGATCCGACCTGGG
AGGACCGATTCCAGGCCGCTCACCATGATCATGCTCATACCCACTGCCACGATGGTTT
GAGGAGTGGCAGGCCGAGCTGAAGGGAAGCGGGGCACTGACTGACGACTTCAAAAACTC
CTTTGTGGAAGCCTTATGTCTAGTGGTCTTGAACCTGTTCCACAGCTGAGGGGAAGGTGG
AGAGTGTGACTGCAAGATCCCCACTCACCACCAAGTCTTATCTGGCTGCTCCCCGAGGTGCC
TGCTACGGGGCTGACCATGACCTGGGCCGCTGCACCTTGTGTGATGGCTCTCTTGAAGGC
CCAGAGCCCCATCCCCACCTCTATCTGACAGGCCAGGATATCTTCACTGTGGACTGGTGG
GGGCCCTGCAAGGTGCCCTGCTGTGACGACGCGCCATCTGGAAGCGGAATCTGTACTCAGAC
CTTAAGAATCTTGATTTCTAGGATCCGGGACAGAGAAGAAAGAAAT**TAGT**TCCATCAGGGAGG
AGTCAGAGGAATTTGCCCAATGGCTGGGGCATCTCCCTTGACTTACCCATAATGCTTTCTG
CATTAGTTCCATTGACAGTATAAAGCACTCTAATTTGGTTCTGATGCTGAAGAGAGGCTGAG
TTTTAAATCAACAATCCGAATCTGGGGCAATGGAATCACTGCTTCCAGCTGGGGCAGGTGAG
TCTTTACGCCCTTTTATAACATGCCATCCCCACTAATAGGATATGACTTGGATAGCTTTGATG
TCTCATCAGCAGCGGGCGCTCTGCATCCCTCACCATGCTCTTCACTGATGATCAAGCGA
ATATTCCATCTGTGGATAGAACCCCTGGCAGTGTGTGACGCTCAACCTGGTGGGTCTAGTTC
TGTCTCAGGCTCTGTCTCTCATTCTTTAGTGTCTACGCTGCACAGTTCTACACTGTCAAGG
GAAAGGGGAGACTAATAGGGCTTAACTCAAACCTGGGCGTGGTGTGGTTGCCATTCCATA
GGTGTGCTGCTGCGCAGTGTGGTTCTGGAGCTTTGGGGTAACAGCAGGATCCATCAGTTAGTA
GGGTGCATGTCAGATGATCATCAATTCATATGGAAGTCCGGGTCTGTCTTCTCTTATCA
TCGGGGTGGCAGCTGGTTCTCAATGTGCCAGCAGGAGTCACTACCTGAGCCCTCAATCAAGC
CTTATGCCCAAATACACAGGAAGGTTGATGCGGGAAGGGTGCAGATCAGGACTCAGGGGA
TGGACTGGTAAGATGAATATCTTGTGGGCTGAAGCAGGCTGCAGGGCATTCAGGCCAAGGG
CAGACAGGGGACAGTGCAGGAGGTGTGGGGTAAGGAGGGAAGTGCACATCAGAAAGGGA
AAGCCACGGAATGTGTGAAGCCAGAAATGGCAATTTGCACTTAATAGCACATGTGAGGG
TTAGACAGGTAGGTGAATGCAAGCTCAAGGTTTGGAAAAATGACTTTTCAGTTATGCTTTG
GTATCAGACATACGAAAGGTCTCTTGTAGTTCGTGTTAATGTAACATTATAAATTTATTG
ATTCCATTGCTTTAAAAAATAAAAAA

MWLPVLVLLAVLLAVLCKVYLGLFGSSSPNPFSEDKVRPPAPLVTDEAKRKVLKQAFSAN
QVPEKLDVVVIGSGFGGLAAAILAKAGKRVLVLEQHTKAGGCCHTFGKNGLEFDTGIHYIG
RMEEGSIGRFILDQITEGQLDWAPLSSPFDIMVLEGPNGRKEYPMYSGEKAYIQGLKEKFPQ
EEAIIIDKYIKLVKVSSGAPHAILLKFLPLPVVQLLDRCGLLTRFSPFLQASTQSLAEVLQQ
LGASSELQAVLSYIFPTYGVTPNHSAFMSHALLVNHYMKGGFYPRGGSSEIAFHTIPVQIRA
GGAVLTATKATVQSVLLDSAGKACGVSKGHLELVNIYCPVVSNAGLFNTYEHLLPGNARCLP
GVKQQLGTVRPGLGMTSVFICLRGTKEDLHLPSTNYYVYDYDMDQAMERYVSMFREEAAEH
IPLFFAFPSAKDPTWEDRFGRSTMIMLIPTAYEWFEEWQAEKKGKRGSDYETFKNSFVEA
SMSVVLKLPFQLEGGKVESVTAGSPLTNQFYLAAPRGACYGADHDLGRLHPCVMASLRAQSPI
PNLYLTGQDIFTCGLVGLAQALLCSSAILKRNLYSDLKNLDSRIRAOKKKN

FIGURE 65

GCAGCGGCGAGGCGGCGGTGGTGGCTGAGTCCGTGGTGGCAGAGGCGAAGGCGACAGCTCTA
 GGGGTGGCACCGGCCCCGAGAGGAGG**ATG**CGGGTCCGGATAGGGCTGACGCTGCTGCTGTG
 TCGGGTGTCTGCTGAGCTTGGCCTCGGCGTCTCGGATGAAGAAGGCAGCCAGGATGAATCCT
 TAGATTCCAAGACTACTTTGACATCAGATGAGTCAGTAAAGGACCATACTACTGCAGGCAGA
 GTAGTTGCTGGTCAAATATTTCTTGATTGAGAAGAATCTGAATTAGAATCCTCTATTCAAGA
 AGAGGAAGACAGCCTCAAGAGCCAAGAGGGGAAAGTGTACAGAAAGATATCAGCTTCTTAG
 AGTCTCCAATCCAGAAAACAAGGACTATGAAGAGCCAAGAAAGTACGGAACCAGCTTTG
 ACCGCCATTGAAGGCACAGCACATGGGGAGCCCTGCCACTTCCCTTTTCTTTCTTAGATAA
 GGAGTATGATGAATGTACATCAGATGGGAGGGAAGATGGCAGACTGTGGTGTCTACAACCT
 ATGACTACAAAGCAGATGAAAAGTGGGCTTTTGTGAACTGAAGAAGAGGCTGCTAAGAGA
 CGGCAGATGCAGGAAGCAGAAATGATGTATCAAACCTGGAATGAAATCCTTAATGGAAGCAA
 TAAGAAAAGCCAAAAAGAGAAGCATATCGGTATCTCCAAAGGCAGCAAGCATGAACCATA
 CCAAAGCCCTGGAGAGAGTGTATATGCTCTTTTATTGGTGATTACTTGCCACAGAATATC
 CAGGCAGCGAGAGAGATGTTTGAGAAGCTGACTGAGGAAGGCTCTCCCAAGGGACAGACTGC
 TCTTGCGCTTCTGTATGCCTCTGGACTTGGTGTAAATCAAGTCAGGCAGGAAGGCTCTGTAT
 ATTATACATTTGGAGCTCTTGGGGCAATCTAATAGCCACATGGTTTTGGTAAAGTAGACTT
TAGTGGAAGGCTAATAATATTAACATCAGAAGAATTTGTGGTTTATAGCGGCCACAACCTTTT
 TCAGCTTTCATGATCCAGATTTGCTTGTATTAAGACCAATATTCAGTTGAACCTCCTTCAA
 ATTCCTTGTTAATGGATATAACACATGGAATCTACATGTAATGAAAGTTGGTGGAGTCCACA
 ATTTTTCTTTAAATGATTAGTTTGGCTGATTGCCCTAAAAAGAGAGATCTGATAAATGGC
 TCTTTTAAATTTTCTCTGAGTTGAATTGTGAGAATCATTTTTACATTAGATTATCATAA
 TTTTAAAAATTTTCTTTAGTTTTTCAAATTTTGTAAATGGTGGCTATAGAAAAACAACAT
 GAAATATTATACAATATTTTGAACAATGCCCTAAGAATTGTTAAATTCATGGAGTTATTT
 GTGCAGAATGACTCCAGAGAGCTCTACTTCTGTTTTTTACTTTTCATGATTGGCTGTCTTC
 CCATTTATTTCTGGTCATTTATTGTCTAGTGACACTGTGCCTGCTCCAGTAGTCTCATTTTCC
 CTATTTTGCTAATTTGTTACTTTTTCTTTGCTAATTTGGAAGATTAACCTATTTTAAATAAA
 ATTATGCTCTAAGATTAAAAA
 AA

FIGURE 66

MRVRIGLTLLLCAVLLSLASASSDEEGSQDESLSKTTLTSDSVKDHTTAGRVVAGQIFLD
SEESELESSIQEEDSLKSQEGESVTEDISFLESPNPENKDYEEPKKVRKPALTAIEGTAHG
EPCHFPPFLFLDKEYDECTSDGREDDGRLWCATTYDYKADEKWGFCETEEEAARRMQEAEEM
YQTGMKILNGSNKKSQKREAYRYLQKAASMNHTKALERSYALLFGDYLQNIQAAREMF EK
LTEEGSPKGQTALGFLYASGLGVNSSQAKALVYYTFGALGGNLIAMVLVSRL

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FIGURE 67

CTTCCAGCCCTGTGCCCAAGCACCTGGAGCATATAGCCTTGCAAACTTCTACTTGCCT
GCCTCCCTGCCTTGTGCCATGGCCTGCCGGTGCCTCAGCTTCTCTGATGGGGACCTTCCT
GTCAGTTTCCAGACAGTCTTGCCCCAGCTGGATGCACTGCTGGTCTTCCAGGCCAAGTGG
CTCAACTCTCTGCACGCTCAGCCCCAGCACGTACCATCAGGGACTACGGTGTGTCTTG
TACCAGCAGCGGGCAGGCAGTGCCCTCGATATCTCTCTACTACCGCTCGGAGGAGGATCA
CCACCGGCCTGCTGACATCCCGATCGATTCTCGGCAGCCAAGGATGAGGCCACAATGCCT
GTGTCTCTACCATTAGTCCCGTGCAGCCTGAAGACGACGCGGATTACTACTGCTCTGTTGGC
TACGGCTTTAGTCCCTAGGGGTGGGTGTGAGATGGGTGCCCTCCCCTCTGCCTCCCATTCT
GCCCTGACCTTTGGTCCCTTTTAAACTTTCTCTGAGCCTTGCTTCCCCTCTGTAAATGGG
TTAATAATATTCAACATGTCAACAAC

FIGURE 68

MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAG
SAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVPEDDADYYCSVGYGFSF

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FIGURE 69

GCGGCCCGCCCCGAGACCGGGGCCCGGGGCGCGGGGCGCGGGGATGCGGCGCCCCGGGGCGG
 CGATGACCGCGGAGCGCAGCGCGCGGGGCCCGGCCCTGACCCGCGCCCGCCCGCTGAGCCCC
 CCGCGCGAGGTCCGGACAGGCCGAG**ATG**ACGCGCGAGCCCCCTGTTGCTGCTCTGCTGCGCGC
 CGCTGCTGCTGGGGGGCTTCCACCGCGCGCGCGCGCGCCGAGGCGCCCCAAAGATGGCGGAG
 AAGTGGTCCACGACGAGGTGGCCGGCTGGGCGCACTGTGCGGCTGCAGTGCCAGTGGAG
 GGGGGACCGCGCGCGCTGACCATGTGGACCAAGGATGGCGCGCATCCGACGAGCGCTGGA
 GCGGCTTCCGCGTCTGCGCGAGGGGCTGAAGGTGAAGCAGGTGGAGGCGAGGATGCGGGC
 GTGTACGTGTGCAAGGCCACCAACGGCTTCGGCAGCGCTGAGCGTCAACTACACCCTCGTCTGT
 GCTGGATGACATTAGCCAGGGAAGGAGAGCTTGGGCGCCGACAGCTCCCTCTGGGGGTCAAG
 AGGACCCCGCGAGCAGTGGGCGACGCGCGCTTACACAGGCCCTCAGCATGAGGCGC
 CGGGTGATCGCACGCGCCGTGGTACTCGCTGCGGCTCAAGTGGCTGGCCAGCGGCGACCC
 TCGGCCCGACATCAGTGGATGAAGGACGACCAAGGCTTACGCGCGCCAGAGGCGCGCTGAGC
 CCAGGAAGAAGAAGTGGACACTGAGGCTGAAGACCTGCGGCGCGGAGGACAGCGGCAAAATAC
 ACCTGCGCGGTGTGCAACCGCGCGGGCGCGCATCAACGCCACCTACAAGGTGGATGTGATCCA
 GCGGACCCGTTCCAAGCCCGTGTCTACAGGCACGCGCCCGTGAACACGACGGTGGACTTCG
 GGGGGACCACTCTTCCAGTGCAAGGTGCGCAGCGAGCTGAAGCCGGTGTACAGTGGCTG
 AAGCGCGTGAGTACGGCGCGGAGGCGCGCCACAACCTCACCATCGATGTGGGCGGCCAGAA
 TTTGTGGTGTGCTGCCACGGGTGACGTGTGCTCGCGGCGCGACGGCTCTTACCTCAATAAGC
 TGCTCATACCCGTTGCCCGCAGGACGATGGGGCATGTACATCTGCTTCCCTGCGCCCAACAC
 ATGGGCTACAGCTTCCGACGCGCTTCTTCCAGCTGTGCGGACAGCCAAACCGCGCAGGGCG
 GCTTGGGCTCTCTGCTCTCGGCCACTAGCTTGGCTGGCCGTGGTGTCTATCGGCATCCGAG
 CGGGCGCTGTCTTATCTTGGGACACCTTGTCTGTGCTTGGCAGCGCCAGAGAAGACCGG
 TGCACCCCGCGCTTCCCTTCCCTTGGCTGGGACCGCGCGCGGGGCGGGCGCGCGCGCGC
 CAGCGGAGACAAGAGCTTCCCTGCTTGGCGCGCTCAGCGCTGGCCCTTGGTGTGGGCGTGT
 GTGAGGAGATGGGTCTCTCGCGAGCCCCAGCACTTATGGGCCCGAGGCCAGTGTGCTGGC
 CCTAAGTTGTACCCCAAACCTTACACAGACATCCACACACACACACACACACTCTCACAC
 ACATCACACGTGGAGGGCAAGGTCCACAGCACATCCACTACGTGCT**TAG**AGCGGCCGCT
 ATCTGAGTGGGCGAGGGGGGGCGGCCAGACAGGCAGACTGGGAGGATGGAGGACGGAGCT
 GCAGACGAAGCGAGGCGGCTATGGCGAGGAGGAATGGCCAGCACCAGGCGAGTCTGTGTG
 TGAGGCATGACCCCTGGACACACACACACACACACACTACCTGGATGCTGTATGTCAC
 ACACATGCGCGCACACGTGCTCCCTGAAGGCACACGTACGCACACGCACATGCACAGATATG
 CCGCCTGGGACACAGATTAAGCTGCCAAATGCAAGCACACGCACAGACAGATGCCAGAAACA
 TACAAGGACATGCTGCCCTGAACATAACACAGCACACCATGCGCAGATGTGCTGCCTGGACA
 CACACACACACACAGGATATGCTGTCTGGACGCACACAGCTGCAGATATGGTATCCGGACACA
 CAGCTGCAGATATGCTGCCTGGACACACAGATAATGCTGCTTACACACACATGCGCGGACCG
 ATATTGCTGGACACACACACACACACCGCTGCACAGATATGCTGTCTGGACACGCACAC
 AATGGCAGATATGCTGCCTGGACACACACTTCCAGACACAGCTGCACAGGCGAGATATGCT
 GCCTGGACACACGAGATATGCTGTCTAGTCAACACACACACGACAGACATGCTGTCCGGACAC
 ACACACGATGCACAGATATGCTGTCCGGACACACACGCGAGATATGCTGTGCTGGAC
 ACACACAGATATGCTGCCTCAACACTACACACAGTGCAGATATGCTGTGGACACACACA
 TGTGCAGATATGCTGTCTGGACATGCTACACACAGTGCAGATATGCTGTCCGGATACACAGC
 CAGCACACATGACAGATATGCTGCCTGGGACACACTTCCGGACACACATGCACACAGGTT
 GCAGATATGCTGCCTGGACACACACAGATAATGCTGCCTCAACACTACACACAGTGCAGATA
 TATTGCTGGACACACATGTGCACAGATATGCTGTCTGGACATGCACACAGTGCAGATA
 TGTGTCCGGATGCACACGCGACGACACATGCAGATATGCTGTGCTGGGACACACTTCCGGA
 CACACATGCACACAGGTTGCAGATATGCTGCCTGGACACACGCACTGACCTGCTTGGT
 GAGGGTGTGCGCTGAGGCTGCACTGCTGCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT
 CCCTGCTCCACCGTCACTCCCCCACTCTGCCCGCTCTGTCCCCGCTCAGTCCCCCGCTT
 CATCCCCGCTCTGTCCCCCTGGGCTTGGCGGCTATTTTGGCACCTGCTTGGGTGGCCAGG
 AGTCCCCCTACTGCTGTGGGCTGGGGTGGGGGACAGCAGCCCCAAGCCTGAGAGGCTGGAG
 CCGATGGCTAGTGGCTCATCCCCAGTGCATTCTCCCCGTGACACAGAGAGGGGCGCTTGGTA
 TTTTATTTTAAAGAAATGAAGATAATATTAATAATGATGGAAGGAAGACTGGGTGTGACAGGAC
 TGTGGTCTCTCTGGGGCGCGGACCGGCTGGTCTTTCAGCCACTGCTGATGACCAACCCCG
 GTCCAGGCCAGACACACCCCCACCCCACTGTGCTGGTGGCCCCAGATCTCTGTAATTTTA
 GTAGAGTTTGAGCTGAAGCCCCGTATATTTAATTTATTTGTTAAACAAAA

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FIGURE 70

MTPSPLLLLLLPPLLLGAFPPAAAAARGPPKMADKVVPRQVARLGRTVRLQCPVEGDPPLTM
WTKDGRTIHSGWSRFRVLPQGLKVKQVEREDAGVYVCKATNGFGSLSVNYTLVLDDISPGK
ESLGPDSSSGQEDPASQQWARPRFTQPSKMRRRVIARPVGSSVRLKCVASGHPRPDITWMK
DDQALTRPEAAEPRKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQRTRSKPVL
TGTHPVNTTVDFGGTTSFQCKVRSDVKPVIQWLKRVEYGAEGRHNSTIDVGGQKFVVLPTGD
VWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLTVPDPKPPGPPVASSSSA
TSLPWPVVIGIPAGAVFILGTL LLWL CQAQKKPCTPAPAPPLPGHRPPGTARDRSGDKDLPS
LAALSAGPGVGLCEEHGSPAAPQHLLGPGPVAGPKLYPKLYTDIHTHTHSHTHSHVEGKV
HQHIIHYQC

[illegible]

FIGURE 72

MVGTAKAWVFSFLVLEVTSVLGRQTMLTQSVRRVQPGKKNPSIFAKPADTLESFGIEWTTFWNI
DYPGGKGDYERLDAIRFYYGDRVCARPLRLEARTTDWTFAGSTGQVHVHSGPREGFWCLNREQ
RPGQNCSNYTVRFLCPCPGSLRRDTERIWSPWSPWSKCSAACGQTGVQTRTRICLAEMVSLCS
EASEEGQHCHMGQDCTACDLTCPMGQVNADCDACMCQDFMLHGAVSLPGGAPASGAIIYLLT
TPKLLTQTDSGGRFRIPGLCPDGKSLIKITKVKFAPIVLTMPKTSLKAATIKAEFVRAETPY
MVMNPETKARRAGQSVSLCCKATGKPRPDKYFWYHNDTLLDPSLYKHESKVLRLKQQHAG
EYFCAGQSDAGAVKSKVAQLLVITASDETPCNPVPESEYILRLPHDCFQNCATNSFYDDVGRCPV
KTCCAGQDNMIRCDVAGQNCGISKTEEREIQCSGYTLPTKVAKCESQCRTETRSYIVGRV
SAADNGEPMRFGHVYMGNSRVSMTGKGTTLHVPQDTERLVLTFDVRLQCFVNTTKVLPFN
KKGSAVFHEIKMLRRKEPITLEAMETNIIPLGEVVGEDPMAELEIPSRSFYRQNGEPYIGKV
KASVTFLDPRNISTATAAQTDLNFINDEGDTFPLRTYGMFSVDFRDEVTSEPLNAGKVKVLH
DSTQVKMPEHISTVKLWSLNPDTGLWEEEGDFKFENQRRNKRDRFTVLVGNLEIRERRFLNL
DVPESRRCFVKVRAIRSERFLPSEQIGGVISVINLEPRTGFLSNPRAWGRFDSVITGPNGA
CVPAPCFDDQSPDAYSAYVLASLAGEELQAVESSPKFNPNAIGVPPYLNKLNYYRRTDHEDPR
VKKTAFQISMAKFRPNPNSAEESNGPIYAFENLRACEEAPSAAHFRFYQIEGDRYDNTVPFN
EDDPMSWTE DYLAWWPKPMEFRACYIKVKIVGLEVNVRSRNMGGTHRRTVGKLYGIRDVRS
TRDRDQPNVSAACLEFKCSGMLYDQDRVDRTLKVVI PQGSCRRASVNPMLHEYLVNHLPLAV
NNDTSEYTM LAPLDPLGHNYGIYTVTDQDPRTAKEIALGRCFDGTSDGSSRIMKSNVGVALT
FNCVERQVGRQSAFYQLQSTPAQSPAAGTVQGRVPSRRQQRASRGGRQGGVVASLRFPRVA
OQPLIN

FIGURE 73

CTGCAAGTTGTTAACGCTAACACACAAGTATGTTAGGCTTCCACCAAAGTCTCAATATACCTGAATACGCAC
AATATCTTAACCTTCATATTTGGTTTTGGGATCTGCTTTGAGGTCCCATCTTCATTTAAAAAAAATACAGAG
ACCTACCTACCCGTACGCATACATATGTGTATATATGTAACTAGACAAGAATCCGAGATCATAAAGC
AAGCTCTGCTTTAGTTTCCAAGAGATTACAAAGAATTTAGAGATGATTTGTCAAGATCCCTCTGCATTATG
CCCTTTGGGTTACGGTGTCTCAGTGATGCAGCCCTACCCTTTGGTTTGGGGACATTATGATTTGTGTAAAGCT
CAGATTTACACGGAAGAGGAAAGTTTGGGATTACATGGCTGCAGCCGGAATCCACGCATACACAAAATA
TCTGAAAGTGAAGACTCGATCTCCGGATATTACCTGTGGAGACCCCTCTGAGACGTTCTGTGCAATGGGCAATC
CCTACATGTGCAATAATGAGTGTGATGCGAGTACCCCTGAGCTGGCACACCCCTGAGCTGATGTTTGAATTT
GAAGGAAGACATCCCTCCACATTTTGGCAGCTGCCACTTGGGAAGGATATCCCAAGCCTCTCCAGGTTAATCAT
CACTCTGTCTTGGAGCAAAACCATTGAGCTAACAGACAACATAGTTATTACCTTTGAATCTGGGCGTCCAGACC
AAATGATCCTGGAGAAGTCTCTCGATTATGGACGAACATGGCAGCCCTATCAGTATTATGCCACAGACTGCTTA
GATGCTTTTACATGGATCCTAAATCCGTGAAGGATTTATCACGCATACGGTCTTAGAAATCATTGACACAGA
AGAGTACTCAACAGGATATACAACAATAGCAAAATATCCACTTTGAAATCAAAGACAGGTTCCGCGCTTTTG
CTGGACCTCGCCTACGCAATATGGCTTCCCTCTACGGACAGCTGGATACACCAAGAACTCAGAGATTTCTTT
ACAGTCAACAGACTGAGGATAAGGCTGTTAAGACAGGCCGTTGGGGAATATTTGTAGATGAGCTACACTTGGC
ACGCTACTTTTACGCGATCTCAGACATAAAGGTGCGAGGAAGGTGCAAGTGTAACTCCATGCCACTGTATGTG
TGTATGACACACAGCAAAATTGACATGCGAATGTGAGCACAACTACAGGTCCAGACTGTGGGAAATGCAAGAAG
AATATACAGGGCCGACCTTGGAGTCCAGGCTCCTATCTCCCATCCCCAAAGGCACTGCAAAATACCTGTATCCC
CAGTATTTCCAGTATTTGGTAGCAATGTCTGCGACAACGAGCTCCTGCACTGCCAGAACGGAGGACGTGCCACA
ACAACGTGCGCTGCTGTGCCCGGCGCATACACGGGCATCCTCTGCGAGAAGCTGCGGTGCGAGGAGCTGGC
AGCTGCGGCTCCGACTTGGCCAGGGCGCGCCCCGCGACGGCACCCCGAGCGTGTCTGCTGCTGACACGCTGTCT
GGGAACGGCCAGCCCTTGGTTGTTCTAGGTGTACCTCCAGCCACACGGACGGGCTGTGCGGTGGGGAAGCA
GACACAACCCAAACATTTGCTACTTAACATAGGAACACACACATACAGACACCCCATCAGACAGTGTACAAA
CTAAGAAGGCTTAACCTGACTAAGCATATTTATCACCCCTGGACAGCATCCAGTCAAGACTGTTAAATTC
TGACTCCAGAGGAGTTGGCAGCTGTTGATATTATCACTGCAAAATCATTGCCAGCTCAGAGCATATTGTGGA
TTGGAAGGCTGCGACACGCCCCCAACAGGAAGACAAAAACAACAAATCAACCGACTAAAACATTTGCG
TACTCTAGCCTGGTGGCGCCCTAGTAGCACTCCGCCAGTGTGTGGACCAACCAATAGCAATTTCTTGTCTGTCAG
GTGATTTGGGCATTAAGCAAAATCTGTACAAAGCTGCCATATTGSCCTGCTCCGTCCCTGAATCCCTTCAAC
CTGTGCTTTAGTGAACGTTGCTCTGTAAACCTCTGTTGTTGAAAGATTTCTTGTCTGATCTAGTAGTGACA
TGTGTAACAGCCCCCTCTAAAGCGCAAGCCAGTATACCCCTGTATATCTTAGCAGCACTGAGTCCAGTGGCA
GCACACACCCCATATACAAAGATGGCTATAGGAAAAAGAAAGTGTATCTATCCTTTGTATTTCAAATGAAGTT
ATTTTTCTTGAACTACTGTAATATGTAGATTTTTTGTATTTATGCAATTTGTGTCTCCAGCAATCTGTGTAAT
GTATCTAATTCGAATCAGCAAGAGCTGACATTTTATTTTGTCTCTTTCGTTGCTTTGCTTCTGCTGTCGAGA
GATTTCTCTGTAAGGGCAACGAACGTGCTGGCATCAAAGAATATCAGTTTACATATATAACAAGGTGAATAAGA
TTCCACCAAGGACATTTCTAAATGTTTTCTTGTGCTTTAACACTGGAAGATTTAAAGAAATAAAACTCCTGCA
TAAACGATTTCAGGAATTTGTATGCAATTTCTTAAGATGAAGGAACAGCCACCAAGCAGTTTTCACACTCACT
TTACTGATTTCTGTGTGAGCTGACATTTAGCTGACGAATTTAGTTCCCGGAAGATGGATTGATGTTCAC
AGCTTGACACACTTTCTGCAAAATATGAGACTATTTCCACTTGGGAAAAATTACACAGCAAAAAA

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FIGURE 74

MYLSRSLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMACQPESTDMTKYLK
VKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELAHPPPELMFDFEGRHPSTFWQSATWK
EYPKPLQVNITLSWSKTIELTDNIVITFESGRPDQMLEKSLDYGRTWQFYQYYATDCLDAF
HMDPKSVKDLSQHTVLEICTEEYSTGYTTNSKIIHFEIKDRFALFAGPRLRNMASLYGQLD
TTKKLRDFFTVTDLRIRLLRPVAGEIFVDELHLARYFYAISDIKVRGRCKCNLHATVCVYDN
SKLTCECEHNTTGPDCGKCKKNYQGRPWSPGSYLPIPKGTANTCIPSISSIGTNVCDNELLH
CQNGGTCHNNVRCLCPAAYTGILCEKLRCEEAGSCGSDSGQGAPPHGTPALLLLTTLLGTAS
PLVF

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CCACGCGTCCGGGTGACCTGGGCCGAGCCCTCCGGTCGGCTAAGATTGCTGAGGAGCGGCCG
CGGGTAGCTGGCAGGCGCCGACTTCCGAAGGCCGCCGTCGGGGCAGGTTGCTCTCATGACTT
CTCTTGTGGACC**ATG**TCGCGTATCTTTTTTGCTGCGTGGTACGGGTAAGGGATGGACTGCC
CCTCTCAGCCTCTACTGATTTTTACCACACCCAAGATTTTTTGAATGGAGGAGACGGCTCA
AGAGTTTAGCCTTGCAGCTGGCCAGTATCCAGGTGCAGGTTCTGCAGAAGTTGTGACTTT
AGTATACATTTTTCTTCTTCGGGGACGTGGCCTGCATGGCTATCTGCTCCTGCCAGTGTCC
AGCAGCCATGGCCTTCTGCTTCTGGAGACCTGTGGTGGGAATTCACAGCTTCCTATGACA
CTACCTGCATTGGCCTAGCCTCCAGGCCATACGCTTTTTCTGAGTTTGACAGCATATTAG
AAAGTGAAGTGGCATTTTAACTATGTAAGTTCCTCTCAGATGGAGTGCAGCTTGGAAAAAT
TCAGGAGGAGCTCAGTTGCAGCCTCCAGCGGTTCTACTCTGGAGGACACAGATGTGGCAA
ATGGGGTGATGAATGGTACACACCGATGCACCTGGAGCCTGCTCCTAATTTCCGAATGGAA
CCAGTGACAGCCCTGGGTATCCTCTCCCTCATTCTCAACATCATGTGTGCTGCCCTGAATCT
CATTGAGGAGTTACCTTGCAGAACATTCTTTACAGGATCCAGGAGCTGGTTCTGCTGGT
TGGACCAAACTCTG**TGA**GCCAGCCACCCCTGACCCAAATGAGGAGAGCTCTGATTCTCCCAT
CCGGGAGCAGTGATGTCAAACCTTCTGCTGCTGGGAAATCTCATCAGCAGGGAGCCTGTGGA
AAAGGCATGTGAGTGAAATCTGGGAATGGCTGGATTGCGAAACATCTGCCCATGTGTATTG
ATGGCAGAGCTGTTGCCCACAGCGCCTTTTATTAGGGTAAAAATTAACAAATCCATTCTAT
TCCTCTGACCCATGCTTAGTACATATGACCTTTAACCCCTTACATTTATATGATTCTGGGGTT
GCTTCAGAAGTGTTATTTTCATGAATCATTTCATATGATTTGATCCCCAGGATTCTATTTTGT
TTAATGGGCTTTTCTACTAAAAGCATAAAATACTGAGGCTGATTTAGTCAGGGCAAAACCAT
TTACTTTACATATTCGTTTTCAATACTTGCTGTTTCATGTTACACAAGCTTCTTACGGTTTTC
TTGTAACAATAAATATTTGAGTAAATAATGGGTACATTTTAACAAACTCAGTAGTACAACC
TAAACTTGATAAAAGTGTGTAAAAATGTATAGCCATTTATATCCTATGTATAAATTAATG
AAGTGGCTTCGAAATGGCAGAATAAATCTAAAGTGTTTATTAACAAAAAAAAAAAAAAAAAAAA
AAAA

FIGURE 76

MSVIFFACVVRVRDGLPLSASTDFYHTQDFLEWRRRLKSLALRLAQYPGRGSAEGCDFSIHF
SSFQDVACMAICSCQCPAAMAFCFLETLWWEFTASYDTTCIGLASRPYAFLEFDSIIQKVW
HFNYVSSSQMECSLEKIQEELKLQPPAVLTLEDTDVANGVMNGHTPMHLEPAPNFRMEPVTA
LGILSLILNIMCAALNLRGVHLAEHSLQDPRSWFCWLDQTS

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FIGURE 77

TGCTTCCTGGAGACCCCTGTGGTGGGAATTCACAGCTTCNTATGACACTACCTGCATTGGCNT
AGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTCAGAAAGTGAAGTGGCATT
TTAACTATGTAAGTTCCTNTCAGATGGAGTGCAGCTTGAAAAAATTCAGGAGGAGCTCAAG
TTGCAGCCTCCAGCGGTTCTCANTATGGAGGACACAGATGTGGCAAATGGGGT

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CTCAGCGCGCTTCCCTGTAAGCGAGCCTAGTGGCGGGTGTGTTGCATTGAAACGTGAGCGCGA
CCCCGACCTTAAAGAGTGGGGAGCAAGGGAGGACAGCCCTTTAAACAGCGAGCGGGTGTG
CTGCTCCCTTTAAAGGCGGGGCGCTCCGAGCACTGTATCTGAGCCCCAGACTGCCCCAGT
TCTGTTCGCAAGGCTGCGAGGAAAGGCCCTAGGCTGGGTCTGGGTGCTTGCGCGCGCGGCTT
CTCCCCGCTCGTCTCTCCCGGGGCCAGAGGCACTCGGCTTCAGTACATGCTGAGCAGAGT**A**
TGGAAGCACTGTACTAGCAAGTGTATCCGTGCGAAGACAGTATTTCCACAGAGAGTACGCG
GAGTGTATTATATCAACACTTCTGTTGCAACACTGTACATCTCTCGCCACATCTTCTCTGA
CCGCTTCAAGAAGCCTGCTGAGTTCACCACAGCTGGATGATGAAGATGCCACCGTCAACAAGA
TGTGCGTCTGAGCTGTGCACTTTACCTTGCAATTGCCCTGGGTGCTGTCTGCTCTGCCCT
TTCTTCATCATCAAGTAAGGTGCTGCTCTCCCTGCTCGGAACATACTACATCAGTGGCT
CAAGGCTCCCTCATCTCATGGGCTCTGGAACCTGTTTTCTCTTCCCAACCTGTCCTTA
TCTTCTCATGCCCTTTCATATTTCTTACTGAGTCTGAGGGCTTGTCTGCGTCCAGAAG
GGTGTCTGGGCGGGGTCTATGAGACAGTGTGTGATGTGTAGCTCCCTACTCTGCTGGTGC
AGGATGTGTGGTGGCATCAGCCATTGTGGAACAAGAACAGGCCAACAGAGAGTCACTCT
ATGACTTTTGGGAGTACTCTCCCTACCTCTACTCATGTCATCTCCTTCTTGGGGTCTG
CTGCTCTGGTGTGTACTCACTGGGTCTCGGCCGATGTTCTCCGTCACCTGGGAAGCTGCT
AGTCAAGCCCGGCTGCTGGAAGCACTGGAGGACAGCTGTACTGCTCAGCCTTTTGGAGG
CAGCCCTGACCCCGAGAGTCTGTAACTCTACTTCTGCTGGCTGCCTTTAGACATGGAGTGT
CTACACAGACAGGTCCTGGCTCTGCAGACACAGAGGCTCTGCTGGAGAAGAGGCCGAAG
TTCAGCCTGGCAACGGAACCTGGGCTACCCCTGGCTATGCTGTGCTTCTGGTGTCTGACGG
CGCTGTCTGTGTCATTTGTGCCATCCACATCTGGAGCTGTCTCATGATGAGGCTGCCAT
CCCCAGGATGTCAGGGTACTCTTATGCCAGGTCTCTCTTCCAGCTGGGCTCTTTGG
TGCGTCACTTCAGGTTGTACTATCTTTTACCTAATGGTGTCTCTCAGTTGTGGGCTTCTATA
GCTCTCCACTTCTCCGAGCCTCGGCCCGAGATGGCAGCAGACTGCCATGAGCAGAGATAAT
GGGAAGTGTGTCTGTCTGCTGGTCTTAAGCTCAGCACTTCTGTCTTCTCTCGAAGCTGGG
GCTCACTCGTGTGTGACTCTGCTGGGTGACTTTGGACGCTTCAACTGGCTGGGCAATTTCTAC
TTGTGTTCTCTTACAACGCACTTTGACGGCTCACCACACTGCTGTGTGGAAGACCTT
ACTGCAGCTGTGCGGGCAGCTGATCCGGGCTTTGGGCTGGACAGACTCCGCTGCCGT
CTCCGGTTTCCCCAGGCATCTAGGAAGCCACGACACAG**TGA**CTCCAGCTGGGGGTGGGA
AGGAAAAAATGGACATGTCATCTGCTGCTTAGGCTGGAGGGAGCCCAAGGCTACTTGG
ACCTCAGGACCTGGAATCTGAGAGGGTGGTGGCAGAGGGGAGCAGAGCCATCTGCACTATT
GCATTAATCTGAGCCAGAGTTTGGACAGGACCTCTCTGCTTTTCCATATCTTAATGTGGCC
CAGCATGGGTGAGGGCTGGGTGACTGGGTCTAGCCCTGATCCCAATCTGTTTACATATCA
ATCTGCTCTGACTGCTGTTCTGGGCCATCCCCATAGCCATGTTTACATGATTGTATGTGCAAT
AGGTTGGGTAGGGGACGGGAAGGACTGGGCCAGGGCAGGCTCGGAGATAGATTGTCTTC
CTTGCTCTGGCCACGACAGAGCTAAGCACTGTGCTATCTGGAGGGGCTTTGGACCACTG
AAGACCAAGGGGATAGGGAGGAGGAGGCTTACGCCATCAGCAATAAAGTTGATCCCAAGGA
AAAAAA

FIGURE 79

MEAPDYEVLSVREQLFHERIRECIISTLLFATLYILCHIFLTRFKKPAEFTTVDDDEDATVNK
IALELCTFTLAIALGAVLLL PFSIISNEVLLSLPRNYIQLNGSLIHGLWNLVFLFPNLSL
IFLMPFAYFFTESEGFAGSRKGVLRVYETVVMLMLLTLLVLGMVWVASAIVDKNKANRESL
YDFWEYYLPYLYSCISFLGVLLLLVCTPLGLARMFSVTGKLLVKPRILLEDLEEQLYCSAFEE
AALTRRICNPTSCWLPDME LLHRQVLALQTQRVLEKRRKASAWQRNLGYPLAMLCLLVLT
GLSVLIVAIHILELLIDEAAMP RGMQGTSLGQVSFSKLGSGFAVIQVVLI FYLMVSSVVG FY
SSPLFRSLRPRWHD TAMTQIIIGNCVCLLVSSALPVFSRTLGLTRFDLLGDFGRFNWLG NFY
IVFLYNAAFAGLTTLCLVKTFTA AVRAELIRAFGLDRLPLPVSGFFQASRKTQH Q

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FIGURE 80

GGCTGCCGAGGGAAGGCCCTTGGGTTGGTCTTGGTTGCTTGGCGGCGGCGGN TTCNTCCCC
GCTCGTCCTCCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGAAGC
ACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGTGTA
TTATATCAACACTTCTGTTTGCAACACTGTACATCCTCTGCCACATCTTCCTGACCCGCTTC
AAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCG

FIGURE 81

GACCGACCTTAAAGAGTGGGAGCAAAGGGAGGACAGAGCCTTTTAAAACGAGGCGGTGGTGC
CTGCCCCTTTAAGGGCGGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCCGAGTTTC
TGTGCGAGGCTGCGAGGAAAGGCCCTAGGCTGGGTCTGGTGCTTGCGGGCGGCGGCTTCCT
CCCCGTTGTCNTCCCCGGGCCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGA
AGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGT
GTATTATATCAACACTTCTGTTTGCAACACTGTACATCNTCTGCCACATCTTCTGACCCGC
TTCAAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGATTGC
GCTCGAGCTGTGCACCTTTACCTGGCAATTGCCCTGGGTGCTGTCCTGCTCCTGCCCTTCT
CCATCATCAGCAATGAGGTGCTGCACTCCC

GATGTGCTCCTTGGAGCTGGTGTGCAGTGTCTGACTGTAAGATCAAGTCCAAACCTGTTTT
GGAATTGAGGAAACTTCTCTTTTGATCTCAGCCCTTGGTGGTCCAGGTCTTCTAGTCTGCTGT
GGGTGATATTACTGGTCTGGCTCTGTCTAGTGGACAGTTTGAAGGACACCCAGGCCCATI
ATTTTCTCTCCAGCTCCATGGACCACAGTCTTCCAAGGAGAGAGAGTGACCCCTCACTTGCAA
GGGATTTCTGCTTCTACTCACCACAGAAAACAAATGGTACCATCTCGGTACCTTGGGAAAGAAA
TACTAAGAGAAACCCAGACAATATCCTTGAGGTTCAAGGAATCTGGAGAGTACAGATGCCAG
GCCAGGGCTCCCTCTCAGTAGCCCTGTGCACTTGGATTTTTCTTTCAGAGATGGGATTTC
TCATGCTGCCCAGGCTAATGTTGAACTCTGGGCTCAAGTGATCTGCTCACCAGCCTCTC
AAAGCGCTGGGATTACAGCTTCGCTGATCTGCAAGCTCCACTTTCTGTGTTTGAAGGAGAC
TCTGTGGTTCTGAGGTGCCGGGCAAGGCGGAAGTAACACTGAATAATACTATTTACAAGAA
TGATAATGTCTTGGCATTCCTTAATAAAGAACTGACTTCCAAAAAAAAAAAAAAAAAAAAA
AAA

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FIGURE 83

MLLWVILLVLAPVSGQFARTPRPIIFLQPPWTTVFQGERVTLTCKGFRFYSPQKTKWYHRYL
GKEILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDIFSSEMGFPHAAQANVELLGSSDLLT

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FIGURE 84

CAGAAGAGGGGGCTAGCTAGCTGTCTCTGCGGACCAGGGAGACCCCCGCGCCCCCGGTGT
 GAGCGGCCCTCACAGGGCCGGGTGGCTGGCGAGCCGACGCGGCGGCGAGGAGCTGTGAG
 GAGTGTGTGGAACAGGACCCGGGACAGAGGAACATGGCTCCGCAGAACCTGAGCACCTTTT
 GCCTGTTGCTGCTATACCTCATCGGGCGGTGATTGCCGGACGAGATTTCTATAAGATCTTG
 GGGGTGCCTCGAAGTGCCCTCTATAAAGGATATTAAAAAGGCCTATAGGAACTAGCCCTGCA
 GCTTCATCCCAGCCGGAACCCCTGATGATCCACAAGCCCAGGAGAAATTCAGGATCTGGGTG
 CTGCTTATGAGGTTCTGTGAGATAGTGAGAAACGGAACAGTACGATACTTATGGTGAAGAA
 GGATTAAGATGGTCAATCAGAGCTCCCATGGAGACATTTTTTACACTTCTTTGGGGATTT
 TGGTTTCATGTTTGGAGGAACCCCTCGTCAGCAAGACAGAAATATTCAGAGGAAGTGATA
 TTATTGTAGATCTAGAAGTCACTTTGGAAGAAGTATATGCAGGAAATTTGTGGAAGTAGTT
 AGAAACAAACCTGTGGCAAGGCAGGCTCCTGGCAAACGGAAGTGCAATTGTGCGCAAGAGAT
 GCGGACCACCCAGCTGGGCCCTGGGCGCTTCCAATGACCCAGGAGGTGGTCTGCGACGAAT
 GCCCTAATGTCAAAGTGTGAATGAAGAACGAACGCTGGAAGTAGAAATAGAGGCTGGGGTG
 AGAGACGGCATGGAGTACCCCTTTATTGGAGAAGGTGAGCCTCACGTGGATGGGGAGCCTGG
 AGATTTACGGTTCGAATCAAAGTTGTCAAGCACCCAAATATTTGAAAGGAGAGGAGATGATT
 TGTACACAAATGTGACAATCTCATTAGTTGAGTCACTGGTTGGCTTTGAGATGGATATTACT
 CACTTGGATGGTCACAAGGTACATATTTCCCGGGATAAGATCACCGAGCCAGGAGCGAAGCT
 ATGGAAGAAAGGGGAAGGGCTCCCCAACTTTGACAACAACAATATCAAGGGCTCTTTGATAA
 TCACCTTTTGATGTGGATTTTCCAAAAGAACAGTTAACAGAGGAAGCGAGAGAAGGTATCAAA
 CAGCTACTGAAACAAGGGTCAGTGCAGAAGGTATACAATGGACTGCAAGGATATTGAGAGTG
 AATAAAATTTGACTTTGTTTAAATAAGTGAATAAGCGATATTTATTATCTGCAAGGTTTTT
 TTGTGTGTGTTTTTGTTTTTATTTTCAATATGCAAGTTAGGCTTAATTTTTTTTATCTAATGA
 TCATCATGAAATGAATAAGAGGGCTTAAGAATTTGTCCATTTCGATTTCGGAAAAGAATGACC
 AGCAAAAGGTTTACTAATACCTCTCCCTTTGGGGATTTAATGTCTGGTGCTGCCGCTGAGT
 TTCAAGAAATTAAGCTGCAAGAGGACTCCAGGAGCAAAAGAAACAAATATAGAGGGTTGGA
 GTTGTTAGCAATTTCAATTCAAAATGCCAACTGGAGAAGTCTGTTTTTAAATACATTTTGTG
 TTATTTTTTA

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FIGURE 85

MAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRASIKDIKKAYRKALQLHPDRNPDDPQ
AQEKFQDLGAAAYEVLSDSEKRRQYDTYGEGLKDGHQSSHGDI FSHFFGDFGFMFGGTPRQQ
DRNIPRGSDIIVDLEVTLEEVYAGNFVEVVRNKPVARQAPGKRKCNCRQEMRTTQLGPGRFQ
MTQEVVCDECPNVKLVNEERTLEVEIEPGVRDGM EYPFIGEGEPHYVDGEPGDLRFRIKVVKH
PIFERRGDDLYTNVTISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLWKKGEGLPNFD
NNNIKGLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQKVYNGLQGY

Important features:**Signal peptide:**

amino acids 1-22

Cell attachment sequence.

amino acids 254-257

Nt-dnaJ domain signature.

amino acids 67-87

Homologous region to Nt-dnaJ domain proteins.

amino acids 26-58

N-glycosylation site.

amino acids 5-9, 261-265

Tyrosine kinase phosphorylation site.

amino acids 253-260

N-myristoylation site.

amino acids 18-24, 31-37, 93-99, 215-221

Amidation site.

amino acids 164-168

TGGGACCAGGGAACCCGGGGCCCCCGGTGGAGNGCCTAACAGGCCGGTGNGTGCACCGAA
GCGGCGGGCGGAGGAGTTTGTAGGATTTTGGAAACAGGACCCGACAGAGGAACCATGGTT
CCGCAAGACNTGAGCANTTTTGCCTGTTGNTGNTATACCTCATCGGGGCGGTGATTGCCGG
ACGAGATTTNTATAAGATTTTGGGGTGCCNAGAGTGCCTTNTATAAAGGATATTTAAAGAG
CCTATAGGAAACTAGCCCTGCAGNTTTATCCCGACCGGAAACCTGATGATCCACAAGCCCAG
GAGAAATTCAGGATTTGGGTGCTGCTTATGAGGTTNTGTGAGATAGTGAGAAACGGAAACA
GTACGATAATTATGGTGAAGAAGGATTAAGAGATGGTNATCAGAGCTCCCATGGAGACATT
TTTTCACATNTTTTGGGGATTTTGGTTTCATGTTTGGAGGAACCCCTNGTCAGCAAGACAGA
AATATTCCAAGAG

FIGURE 88

METVVIVAIGVLATIFLASFAALVLVCRQRYCRPRDLLQRYDSKPIVDLIGAMETQSEPSEL
ELDDVVITNPHIEAILENEDWIEDASGLMSHCIAILKICHTLTEKLVAMTMGSGAKMKTSA
VSDIIVVAKRISPRVDDVVKSMPPLDPKLLDARTTALLSVSHLVLVTRNACHLTGGLDWI
DQSLSAEEHLEVLREAALASEPDKGLPGPEGFLQEQSAI

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FIGURE 89

GCTTCATTTCTCCCGACTCAGCTTCCCACCCTGGGCTTTCGAGGTGCTTTCGCCGCTGTCC
 CCACCACTGCAGCC**ATG**ATCTCCTTAACGGACACGCAGAAAATTGGAATGGGATTAACAGGA
 TTTGGAGTGTTTTCTGTTCTTTGGAATGATTCTCTTTTTTGACAAAGCACTACTGGCTAT
 TGGAATGTTTTATTGTAGCCGGCTTGGCTTTTGTAAATGGTTTAGAAAGAACATTCAGAT
 TCTTCTCCAAAACATAAAATGAAAGCTACAGGTTTTTTCTGGGTGGTGATTTTGTAGTC
 CTTATTGGTTGGCCTTTGATAGGCATGATCTTCGAAATTTATGGATTTTTCTCTTGTTCAG
 GGGCTTCTTTCCTGTCGTTGTTGGCTTTATTAGAAGAGTGCCAGTCCTTGGATCCCTCCTAAAT
 TTACCTGGAATTAGATCATTTGTAGATAAAGTTGGAGAAAGCAACAATATGGTAT**TAA**CAACA
 AGTGAATTTGAAGACTCATTTAAATATTGTGTTATTTATAAAGTCATTTGAAGAATATTCA
 GCACAAAATTAAATTACATGAAATAGCTTGTAATGTTCTTTACAGGAGTTTAAACGTATAG
 CCTACAAAGTACCAGCAGCAAATTAGCAAAGAAGCAGTGAAAACAGGCCTTCTACTCAAGTGA
 ACTAAGAAGAAGTCAGCAAGCAAACTGAGAGAGGTGAAATCCATGTTAATGATGCTTAAGAA
 ACTCTTGAAGGCTATTTGTGTTGTTTTCCACAATGTGCGAAACTCAGCCATCCTTAGAGAA
 CTGTGGTGCCGTGTTCTTTCTTTTATTTTGAAGGCTCAGGAGCATCCATAGGCATTTGCT
 TTTTAGAAGTGTCCACTGCAATGGCAAAAATATTTCCAGTTGCACTGTATCTCTGGAAGTGA
 TGCATGAATTCGATTGGATTGTGTCATTTTAAAGTATTTAAACCAAGGAAACCCCAATTTTG
 ATGTATGGATTACTTTTTTTTGNGCNCAGGGCC

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FIGURE 90

MSISLTDQKIGMGLTGFGVFFLFFGMILFFDKALLAIGNVLFVAGLAFVIGLERTFRFFQK
HKMKATGFFLGGVFFVLIGWPLIGMIFEIYGFFLLFRGFFPVVVGFIIRRVPLGSLNLPGI
RSFVDKVGESNNMV

Important features:

Transmembrane domains:

amino acids 12-30 (typeII), 33-52, 69-89 and 93-109

N-myristoylation sites.

amino acids 11-16, 51-56 and 116-121

Aminoacyl-transfer RNA synthetases class-II protein.

amino acids 49-59

FIGURE 91

GAAGACGTGGCGGCTCTCGCCTGGGCTGTTTCCCGGCTTCATTTCTCCCGACTCAGCTTCCC
ACCNTGGGCTTTCCGAGGTGCTTTCGCCGCTGTCCCACCACTGCAGCCATGATCTCCTTAA
CGGACACGCAGAAAATTGGAATGGGATTAACCGGATTTGGAGTGTTTTCTGTCTTTGGA
ATGATTCTCTTTTTGACAAAGCACTACTGGCTATTGGAAATGTTTTATTTGTAGCCGGCTT
GGCTTTGTAATTGGTTTAGAAAGAACATTCAGATTCTTCTTCCAAAAACATAAAATGAAAG
CTACAGGTTTTTTTCTGGGTGGTGATTTGTAGTCCTTATTGGTTGGCCTTTGATAGGCATG
ATCTTCGAAATTTATGGATTTTTTCTCTTGTTT

FIGURE 92

GGCAGCAGGCTGAACCCAGCCGGCTCCATCTCAGCTTCTGGTTTCTAAGTCCATGTGCCAAA
GGCTGCCAGGAAGGAGACGCCCTTCCTGAGTCTCGGATCTTTCTTCCCTTCTGAAATCTTTGA
CTGTGGGTAGTTATTTATTTCTGAATAAGAGCGTCCACGCATCATGGACCTCGCGGGACTGC
TGAAGTCTCAGTTCCGTGTGCCACCTGGTCTTCTGCTACGTCTTTATTGCCTCAGGGCTAATC
ATCAACACCATTACGTCTTCACTCTCCTCCTCTGGCCCATTAACAAGCAGCTCTTCGGAA
GATCAACTGCAGACTGTCTATTGCATCTCAAGCCAGCTGGTGATGCTGCTGGAGTGGTGGT
CGGGCACGGAATGCACCATCTTCACGGACCCGCGCCTACCTCAAGTATGGGAAGGAAAAAT
GCCATCGTGGTTCTCAACCACAAGTTTGAATTGACTTTCTGTGTGGCTGGAGCCTGTCCGA
ACGCTTTGGGCTGTTAGGGGGCTCCAAGGTCTTGCCCAAGAAAGAGCTGGCCTATGTCCAA
TTATCGGCTGGATGTGGTACTTCACCGAGATGGTCTTCTGTTCGCGCAAGTGGGAGCAGGAT
CGCAAGACGGTTGCCACCAGTTTGCAGCACCTCCGGGACTACCCGAGAAGTATTTTTTCTCT
GATTCACTGTGAGGGCACACGGTTCACGGAGAAGAAGCATGAGATCAGCATGCAGGTGGCCC
GGGCCAAGGGGCTGCCTCGCCTCAAGCATCACCTGTTGCCACGAACCAAGGGCTTCGCCATC
ACCGTGAGGAGCTTGAGAAATGTAGTTTCAGCTGTATATGACTGTACACTCAATTTTCAGAAA
TAATGAAAATCCAACACTGCTGGGAGTCTTAAACGGAAAGAAATACCATGCAGATTTGTATG
TTAGGAGGATCCCACTGGAAGACATCCCTGAAGACGATGACGAGTGTCTCGGCCCTGGCTGCAC
AAGCTCTACCAGGAGAAGGATGCCTTTCAGGAGGAGTACTACAGGACGGGCACCTTCCCAGA
GACGCCCATGGTGCCCCCGCGGCCCTGGACCCTCGTGAAGTGGCTGTTTTGGGCCCTCGC
TGGTGCTCTACCCCTTCTTCCAGTTTCTGGTCAGCATGATCAGGAGCGGGTCTTCCCTGACG
CTGGCCAGCTTCATCCTCGTCTTCTTTGTGGCCTCCGTGGGAGTTGCATGGATGATTTGGTGT
GACGGAATTTGACAAGGGCTCTGCCTACGGCAACTCTGACAGCAAGCAGAACTGAATGACT
GACTCAGGAGGTTGCACCATCCGAAGGGAACCTTGGGGAAGTGGTGGCCTCTGCATATCCT
CCTTAGTGGGACACGGTGACAAAGGCTGGGTGAGCCCCTGCTGGGCACGGCGGAAGTCACGA
CCTCTCCAGCCAGGAGTCTGGTCTCAAGGCCGGATGGGGAGGAAGATGTTTTGTAATCTTT
TTTTCCCATGTGCTTTAGTGGGCTTTGGTTTTCTTTTGTGCGAGTGTGTGTGAGAATGGC
TGTGTGGTGAGTGTGAACCTTTGTTCTGTGATCATAGAAAGGATATTTTAGGCTGCAGGGGAG
GGCAGGGCTGGGGACCGAAGGGGACAAGTTCCTCTTTCATCCTTTGGTGCTGAGTTTTCTGT
AACCCTTGGTTGCCAGAGATAAAGTAAAAGTGCTTTAGGTGAGATGACTAAATTTATGCCTC
CAAGAAAAAAAATTAAGTGCTTTTCTGGGTCAAAAAA

FIGURE 93

MDLAGLLKQSFLCHLVFCYVFIASGLIINTIQLFTLLLPINKQLFRKINCRLSYCISSQLV
MLLEWWSGTECTIFTDPRAYLKYGKENAIVVLNHKFEIDFLCGWSLSERFGLLGSGKVLAKK
ELAYVPIIGWMMWYFTEMVFCSRKWEQDRKTVATSLQHLRDYPKPYFFLIHCEGTRFTEKKHE
ISMQVARAKGLPRLKHLLPRTKGFAITVRSRLNVVSAYVDCITLNFNRNNENPTLLGVLNGKK
YHADLYVRRIPLEDIPEDDDECSAWLHKLKYEKDAFQEYYRTGTTFETPMVPPRRPWTLVN
WLFWASLVLYPFFQFLVSMIRSGSSLTASLILVFFVASVGVGRMIGVTEIDKGSAYGNSDS
KQKLAND

CTGAGGCGGCGGTAGCTGAGGAGGGAGAGTTCGTCGGCGGTGCTCTCGGGCTTTGTGCTCG
GCGCACTCGCTTTCCAGCACCTCAACACGGACTCGGACACGGAAGGTTTTCTTCTGGGGAA
GTAAAGGTGAAGCCAAGAACAGCATTACTGATTCCCAAATGGATGATGTTGAAGTTGTTTA
TACAATTGACATTCAGAAATATATTCCATGCTATCAGCTTTTTAGCTTTTATAATTCTTCAG
GCGAAGTAAATGAGCAAGCACTGAGAAAATATTATCAAATGTCAAAAGAAATGTGGTAGGT
TGGTACAAAATCCGTCGTCATTTCAGATCAGATCATGACGTTTATAGAGAGAGGCTGCTTCACAA
AAACTTGCAGGAGCATTTTTCAAACCAAGACCTTGTTTTCTGCTATTAAACCAAGATATA
TAACAGAAAGCTGCTCTACTCATCGACTGGAACATTCCTTATATAAACCTCAAAAGGACTT
TTTCACAGGGTACCTTTAGTGGTTGCCAATCTGGGCATGTCTGAACAACTGGGTATAAAAAC
TGTATCAGGTTCTGTATGTCACCTGGTTTTAGCCGAGCAGTACAACACACAGCTCTAAAT
TTTTTGAAAGAAGATGGATCCTTAAAGGAGGTACATAAGATAAATGAAATGTATGCTTCATTA
CAAGAGGAATTAAGAGATATATGCAAAAAGATGGAAGACAGTGAACAGCAGCTAGATAAACT
AGATAAGGATGTAAACAGTATTAACAGGAAATTTAGAGAAAGGAGAGGAGCAGAGTACAGG
CAGCAAGAGAGAAGAACATCCAAAAGACCTCAGGAGAACATTTTTCTTGTCAAGGCATTA
CGGACCTTTTTCCAAATTTCTGAATTTCTTCATTCATGTGTTATGTCTTTAAAAAATAGACA
TGTTTCTAAAAGTAGCTGTAACACACCACCATCTCGATGTAGTAGACAATCTGACCTTAA
TGGTAGAACACACTGACATTCCTGAAGCTAGTCCAGCTAGTACACCACAATCATTAAGCAT
AAAGCCTTAGACTTAGATGACAGATGGCAATTCAGAGATCTCGGTTGTTAGATACACAAGA
CAAACGATCTAAAGCAAATCTGGTAGTAGTAACCAAGATAAAGCATCCAAATGAGCAGCC
CAGAAACAGATGAAGAAATTGAAAGATGAAGGTTTTGGTGAATATTCACGGTCTCCTACA
TTTTTGAATCCTTTTAACTTACAAGGAGATTTTTTTATTTGGCTGATGGGTAAAGCCAAACAT
TTCTATGTGTTTTACTATGTTGAGTACTTGCAGTAAGTTTCATTTGTTTTACTATGTTTAC
CTGTTTGCAGTAATACACAGATAACTCTTAGTGCATTTACTTACAAAGTACTTTTTCAAAC
ATCAGATGCTTTTATTCCAAACCTTTTTTTCACCTTTCACTTAAGTTGTTGAGGGGAAGGCT
TACACAGACACATTCTTTAGAATTGGAAAAGTGAGACCAGGCACAGTGGCTCACACCTGTAA
TCCCAGCACTTAGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCC
TGGGCAACGATTTGAGACCATGTCTATTAATAAATAAAATGGAAAAGCAAGAATAGCCTTAT
TTTCAAAATATGGAAGAAATTTATATGAAATTTATCTGAGTCATTAATTAATCTCCTTAAG
TGATACCTTTTGAAGAGTACATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCA
ATAAATTTGCAAAAGCATCATCTAAATTTAAAAAATAAAAAAAAAAAAAAAAAA

FIGURE 95

MEGESTSAVLSGFVLGALAFQHLNTDSDEGFLLEGEVKEAKNSITDSQMDDVEVVYTIIDIQ
KYIPCYQLFSFYNSSGEVNEQALKKILSNVKNVVGWYKFRRHSDQIMTFRERLLHKNLQEH
FSNQDLVFLLLTPSIITESCSTHRLEHSLYKPQKGLFHRVPLVVANLGMSEQLGYKTVSGSC
MSTGFSRAVQTHSSKFFEEEDGSLKEVHKINEMYASLQEELKSICKKVEDSEQAVDKLVKDVN
RLKREIEKRRGAQIQAAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHVSKSS
CNYNHHLDVVDNLTLMEHTDIPEASPASTPQIIKHKALDDDRWFKRSRLDQTQDKRSKA
NTGSSNQDKASKMSSPETDEEIEKMKGFGEYSRSPTF

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FIGURE 96

GGCCAGCGCGCGCGGGAGGGCAGAGTCAAGCCAGCCGAGTCCAGCCGAGCAGCGGACAGCGCAGGGGCGAGC
 CCAAGCAGCGCGCGAGCGACGCCGCCGCCGCCACACCTCTGCGGTCCCAGCGGGCCTGCCACCTCTCCCT
 CTTTCCCCCGCTCCCGCTCGCCGGCCAGTCAAGTTGCCGGTTGCCCGCGGAAACCCCGAGGTCAACCA
 CGCCCGCCTCTGCTTCCCTGGCGCGCGCGCTCCACGCCCTCCTTCTCCCTGGCCGCGCGCTGGACCC
 GGGGACCACTTGTCTGAGCGGAGGCCAGTCTACTTTTCCGCCCGCTCTCCTCCGCTGCTCCGCTCTTCCAC
 CAACTCCACTCTTCTCCCTCCAGCTCCACTCGCTAGTCCCCGACTCCGCCAGCCCTCGGCCCGCTGCCGTAG
 CGCCGCTTCCCGCTCGGTCCCAGAGGTGGGAACCGCTCCGCCCGCGCCGACCAATGACAGGTTGCCGTTCGC
 CGCGCTTCTGTCACCTGGCAGTGTCTAGCGCGCGCGCTGCTGGCTGCCGAGCTCAAGTCCGAAAGTTGCTCGG
 AAGTGCAGCTCTTACGTGTCCAAAGGCTTCAACAAGAACGATGCCCGCTCCAGAGATCAACGGTGATCAT
 TTGAAGATCTGCCCCAGGGTTCTACCTGCTGCTCTCAAGAGATGGAGGAGAAGTACAGCCTGCAAAAGTAAAGA
 TGATTTCAAAGTGTGGTCAGCGAACAGTGAATCATTTGCAAGCTGTCTTTGCTTCAAGTTACAAGAAGTTTG
 ATGAATTTCTCAAAGAACTACTTGAAATGCAGAGAAATCCCTGAATGATATGTTTGTGAAGACATATGGCCAT
 TTATACATGCAAAATTTCTGAGCTATTAAAGATCTCTTCGTAGAGTTGAAACGTTACTACGTGCTGGGAAATGT
 GAACCTGGAAGAAATGCTAAATGACTTCTGGGCTCGCCTCTCGAGCGGATGTTCCGCTGGTGAATCCCACT
 ACCACTTTACAGATGAGTATCTGGAATGTGTGAGCAAGTATACGGAGCAGCTGAAGCCCTTCGGAGATGCTCCT
 CGCAAAATTGAAGCTCCAGGTTACTCGTCTTTTGTAGCAGCCGCTACTTTCGCTCAAGGCTTAGCGGTTGCGGG
 AGATGTCGTGAGCAAGGCTCCGTGGTAAACCCACAGCCGAGTACCCATGCCCTGTTGAAGATGATCTACT
 GCTCCCACTGCGGGGCTCTGCTGACTGTGAAGCCATGTTACAACTACTGCTCAAACTCATGAGAGGCTGTTT
 GCCAACCAAGGGATCTCGATTTGAATGGAACAATTTCAATAGATGCTATGCTGATGTTGGCAGAGAGGCTAGA
 GGGTCTTTCAACATTTGAATCGGTCATGGATCCATCGATGTGAAGATTTCTGATGCTATTATGAACATGCAAG
 ATATAGTGTCAAGTGTCTCAGAAGGTTTCCAGGATGTGAGCCCGCCCAAGCCCTCCAGCTGGACGAAT
 TCTCGTTCCATCTCTGAAAGTGCTTCACTGCTCGCTTCAAGCCACATCCCGCAGGAAACGCCCAACCAAGC
 AGCTGGCACTAGTTTGGACCGACTGGTTACTGATGTCAAGGAGAACTGAACAGGCCAAGAAATTTCTGCTCT
 CCCTCCGAGCAACGTTTGCACAGATGAGAGGATGGCTGCAGGAAACGGCAATGAGGATGACTGTTGGAATGG
 AAAGCCAAAGCAGGTACTGTTTTCAGTGACAGGAAATGGAATTAGCCAAACAGGCCAACCAACAGAGGTCCA
 GGTGACACAGCAAAACAGACATCTGATCCTTCGTCAATCATGGCTCTTCGATGATGACCCAGCAAGATGA
 AGAATGCATACATGGGAACGAGCTGGACTCTTGTATCATGATGATGAAGTAGTGGAGAGGAAGTGGAACT
 GGCTGTGATATCAGCAGTGCCCTTCAAGTGTGACTGATGATGCACTGACCATGCTGGGAAGAGTGCCAAATGA
 GAAAGCCGACAGTGTGCTGCTCCTGGGCAAGGCCCTACCTCCTCACTGTCTTCTGCATCTGTTCTCGG
 TTATGCAGAGAGATGGAGATTAATCTCAAACCTCTGAGAAAGTCTTCAACAAAGTTAAAGGCCACCACTT
 ATCACTTTTCACTCTAGTGACTTGTCTTTTAAATGAATGGACAACAATGTACAGTTTACTATGTGCGC
 CACTGGTTTAAAGAGTGTGACTTGTCTTCTCATTCAGTTTGGGAGGAAAAGGAGCTGTGCATGTAGTGTGT
 TCCTGCTCCCCCAACCATGTTAAACGTGGCTAACAGTGTAGGTACAGAACTAGTTAGTTGTGATTTGTGA
 TTTTATCACTCTATTATTGTTTGTATGTTTTTCTCATTTTCGTTTGGGGTTTTTTTCCAACTGTGATCT
 CGCCTGTGTTTCAAGCAAAACAGGGTCCCTCTTGGCAGTAACATGTACGTATTTCTGAAATATTAAATA
 GCTGTACAGAAGCAGGTTTTATTTATCATGTTATCTTATTAAGAGAAAGCCCAAAAGC

09990427.111401

FIGURE 97

MARFGLPALLCTLAVLSAALLAAELKSKSCSEVRRLYVSKGFNKNDAPLHEINGDHLKICPQ
GSTCCSQEMEKEYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSLNDMF
VKTYGHLYMQNSELFKDLFVELKRYVVGNNLEMLNDFWARLLERMFRLVNSQYHFTDEY
LECVSKYTEQLKPFQDVPRKLLQVTRAFVAARTFAQGLAVAGDVVSKVSVVNPTAQCTHAL
LKMIYCSHCRGLVTVKPCYNYSNIMRGCLANQGDLDFEWNNFIDAMLMVAERLEGPFNIES
VMDPIDVKISDAIMNQDNSVQVSQKVFQGCQPPKPLPAGRISRSISESAFSARFRPHHPEE
RPTTAAGTSLDRLVTDVKEKLKQAKKFWSLPSNVNDERMAAGNGNEDDCWNGKGSRYLF
AVTGNGLANQGNNPEVQVDTSKPDILLRQIMALRVMTSKMKNAYNGNDVDFDISDESSGE
GSGSGCEYQQCPSEFDYNATDHAGKSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

09900427.11401

FIGURE 98

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACAGGCTGAGTATCCT
GACCTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAA
GCAACTTACAGCTGCACCGACAGTTGCGATGAAAGTTCTAATCTCTTCCCTCCTCTGTTG
TGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTGCGCAGAGGCCAC
AGGGACCGAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAATGTGAGTGCAA
AGATTGGTTCTCTGAGAGCCCCGAGAAGAAAATTGATGACAGTGTCTGGGCTGCCAAGAAGC
AGTGCCCTGTGATCATTTCAGGGCAATGTGAAGAAAAAAGACACCAAAGGCACCACAGA
AAGCCAAACAAGCATTCAGAGCCTGCCAGCAATTTCTCAAACAATGTCAGCTAAGAAGCTT
TGCTCTGCCTTTGTAGGAGCTCTGAGCGCCCACTCTTCCAATTAAACATTCTCAGCCAAGAA
GACAGTGAGCACACCTACCAGACACTTCTTCTCCCACTCACTCTCCCACTGTACCCACC
CCTAAATCATTCCAGTGCTCTCAAAAAGCATGTTTTTCAAGATCATTTTGTTTGTTGCTCT
TCTAGTGCTTCTTCTCTCGTCAAGTCTAGCCTGTGCCCTCCCTTACCCAGGCTTAGGCTT
AATTACCTGAAAGATTCCAGGAACCTGAGCTTCTTAGCTAGTGTCATTGAACTTAATGTC
AATCAGGAAGAGTAGCAACAGAGTCAATAAATATTTTAAATGTCAAAAAAAAAAAAAAAAAA

FIGURE 99

MKVLISSLLLLPLMLMSMVSSSLNPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRR
KEMTVSGLPKKQCPDHFKGNVKKTRHQRHHRKPNKHSRACQQFLKQCQLRSFALPL

0990427.11409

FIGURE 100

AATGGCTGTCTTAGTACTTCGCCTGACAGTTGTCCTGGGACTGCTTGTCTTATTCCTGACCT
GCTATGCAGACGACAAACCAGACAAGCCAGACGACAAGCCAGACGACTCGGGCAAAGACCCA
AAGCCAGACTTCCCAAATTCCTAAGCCTCCTGGGCACAGAGATCATTGAGAATGCAGTCGA
GTTTCATCCTCCGCTCCATGTCCAGGAGCACAGGATTTATGGAATTTGATGATAATGAAGGAA
AACATTTCATCAAAGTGACATCCTCAGGACACCCCATGTGGCTCCTGGACAATCCAAGAGCA
GCCAAATCCTGCTTTTCCAGTTTGGCTCCACAAGTCCTCCAGGACAGAGCCCTCAAAGCAAC
TCCCAACGAGTTCTCAGGATTCAGGCTCTGGCTTCAACCAAAACAGAACTCATTTTGAACACC
CTGACTGCATTTTTGCTTTTAAAGTTAGAATAAATATGGCGCTTTGGGATCACATAGTTG
ATGGAGAGGAAA

101/330

FIGURE 101

MAVLVLRLTVVLGLLVLFITCYADDKPKPKDDKPKDDSGKDPKPDFPKFLLSGTEIIEHAVE
FILRSMRSRSTGFMEFDDNEGKHSSK

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FIGURE 102

GGAGCGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTGCCCCAGCGGAAGCACAGCT
CAGAGCTGGTCTGCCATGGACATCCTGGTCCCCTCTCTGAGCTGCTGGTGTCTTCTTAC
CCTGCCCTGCACCTCATGGCTCTGCTGGGCTGCTGGCAGCCCTGTGCAAAGCTACTTCC
CCTACCTGATGGCCGTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAACGGGAG
CTCTTCAGCCAGATAAAAGGGCTTACAGGAGCCTCCGGGAAAGTGGCCCTACTGGAGCTGGG
CTGCGGAACCGGAGCCAACTTTCAGTTCTACCCACCGGGCTGCAGGGTCACCTGCCTAGACC
CAAATCCCCACTTTGAGAAGTTCCTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATAT
GAGCGGTTTGTGGTGGCTCCTGGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGT
GGTGGTCTGCACCTCTGGTGTCTGTGCTCTGTGCAGAGCCCAAGGAAGGTCTGCAGGAGGTCT
GGAGAGTACTGAGACCGGGAGGTTGCTCTTTTTCTGGGAGCATGTGGCAGAACCATATGGA
AGCTGGGCTTCTATGTGGCAGCAAGTTTTCTGAGCCACCTGGAACACATTGGGGATGGCTG
TGCCCTACCAGAGAGACCTGGAAGGATCTTGAGAACGCCAGTTCTCCGAAATCCAATGG
AACGACAGCCCCCTCCCTGAAGTGGCTACCTGTTGGGCCCCACATCATGGGAAAGGCTGTC
AAACAATCTTTCCCAAGCTCCAAGGCACTATTGTCTCTTCCCAGCCTCCAATTAGAACA
AGCCACCCACCAGCCTATCTATCTTCCACTGAGAGGGACCTAGCAGAATGAGAGAAGACATT
CATGTACCACCTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGCAATCTCTAATTCAATC
CCGCCTTGACAGTGA AAAAGCTCTACTTCTACGCTGACCCAGGGAGGAACACTAGGACCC
TGTTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTTGCTCCCAATGTTGTC
CCTTTCCTTCGTTCCCATGGTAAAGCTCCTCTCGCTTTCCTCCTGAGGCTACACCCATGCGT
CTCTAGGAACTGGTCACAAAAGTCATGGTGCCTGCATCCCTGCCAAGCCCCCTGACCTCT
CTCCCACTACCACCTTCTTCTGAGCTGGGGGCACCAGGGAGAATCAGAGATGCTGGGAT
GCCAGAGCAAGACTCAAAGAGGCAGAGGTTTTGTCTCAAATATTTTTTAATAAATAGACGA
AACCAGC

FIGURE 103

MDILVPLLQLLVLLLTLP LHL MALLGCWQPLCKSYFPYLM AVLTPKSNRKMESKKRELFSQI
KGLTGASGKVALLELGC GTGANFQFYPPGCRVTCLDPNPHFEKFLTKSMAENRHLQYERFVV
APGEDMRQLADGSMDVVVCTLVLC SVQSPRKVLQEVRRVLRPGGVLF FWEHVAEPYGSWAFM
WQQVFEPTWKHIGDGCCLTRETWKDLENAQFSEIQMERQPPPLKWLPVGPHIMGKAVKQSF
SSKALICSFPSLQLEQATHQPIYLP LRG T

10447-242660

FIGURE 104

GTGGGATTATTTGAGTGAAGATCGTTTTCTCAGTGGTGGTGAAGTTGCCTCATCGCAGG
 CAGATGTTGGGGCTTTGTCCGAACAGCTCCCCCTCTGCCAGCTTCTGTAGATAAGGGTTAAAA
 ACTAATATTTATATGACAGAAGAAAAAGATGTCATTCCGTAAAGTAAACATCATCATCTTGG
 TCCTGGCTGTTGCTCTCTTCTTACTGGTTTTGACCATAACTTCCTCAGCTTGAGCAGTTTG
 TTAAGGAATGAGGTACAGATTGAGGAATTGTAGGGCCTCAACCTATAGACTTTGTCCCAAA
 TGCTCTCCGACATGCAGTAGATGGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATCTG
 AAGACAGGCTTGGGGGGCCATTGCAGCTATAAACAGCATTGAGCACAACACTCGCTCCAAT
 GTGATTTTCTACATTGTTACTCTCAACAATACAGCAGACCATTCTCCGGTCTGGCTCAACAG
 TGATTCCTGAAAAGCATCAGATACAAAATTGTCAATTTTGACCCTAAACTTTTGGAAGGAA
 AAGTAAAGGAGGATCCTGACCAGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTAC
 TTGCCAATTCTGGTTCCAGCGCAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCA
 AGGTGATATTCTTGCCCTTTACAATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAG
 AAGATTGTGATTGAGCCTCTACTAAAGTTGTATCCGTGGAGCAGGAAACCAGTACAATTAC
 ATTTGGCTATCTTGACTATAAAAAGGAAAGAATTGTAAGCTTTCCATGAAAGCCAGCACTTG
 CTCATTTAATCCTGGAGTTTTTTGTTGCAACCTGACGGAATGGAACGACAGAAATATAACTA
 ACCAACTGGAAAAATGGATGAAACTCAATGTAGAAGAGGGACTGTATAGCAGAACCTTGGCT
 GGTAGCATCACAACACCTCCTCTGCTTATCGTATTTTATCAACAGCACTTACCATCGATCC
 TATGTGGAATGTCCGCCACCTTGGTTCCAGTGTGGAACGATATTCACCTCAGTTGTAA
 AGGCTGCCAAGTTACTCCATTGGAATGGACATTTGAAGCCATGGGAAGGACTGCTTCATAT
 ACTGATGTTTTGGGAAAAATGGTATATTTCCAGACCCAAACAGGCAAATTCAACTTAATCCGAAG
 ATATACCGAGATCTCAAACATAAAGTGAAACAGAATTTGAACTGTAAGCAAGCATTTCTCAG
 GAAGTCTGGAAGATAGCATGCATGGGAAGTAACAGTTGCTAGGCTTCAATGCCTATCGGTA
 GCAAGCCATGGAAAAAGATGTGTGAGCTAGGTAAGATGACAACTGCCCTGTCTGGCAGTC
 AGCTTCCCAGACAGACTATAGACTATAAATATGTCTCCATCTGCCTTACCAAGTGTCTTCTT
 ACTACAATGCTGAATGACTGGAAGAAGAACTGATATGGCTAGTTCAGCTAGCTGGTACAGA
 TAATTCAAAACCTGCTGTTGGTTTTAATTTTGTAACCTGTGGCTGATCTGTAATAAACTT
 ACATTTTTC

FIGURE 105

MSFRKVNIIILVLAVALFLLVLHHNFLSLSSLLRNEVTDSGIVGPQPIDFVPNALRHAVDGR
QEEIPVVIAASEDRLGGAIAAINS IQHNTRSNVIFYIVTLNNTADHLRSWLNSDSLKSIRYK
IVNFDPKLLEGKVKEDPDQGESMKPLTFARFYLPILVPSAKKAIYMDDDVIVQGDI LALYNT
ALKPGHAAAFSEDCDSASTKVIRGAGNQYNYIGYLDYKKERIRKLSMKASTCSFNPGVFVA
NLTEWKRQONITNQLEKWMKLNVEEGLYSRTL AGSITTPLLIVFYQQHSTIDPMWNVRLGS
SAGKRYSPQFVKA AKLLHWNGHLKPWGRTASYTDVWEKWYIPDPTGKFNLIRRYTEISNIK

090909 11444
000000 240660

FIGURE 106

TGGTTTTTGCCCCATAAATCCCTCAGCTTGAGCAGTTTGTTAAGGAATGAGGTTACAGATT
CAGGAATTNTAGGNCCTCAACCTNTAGANTTTGTCCCAAATGTTCTCCGACATGCAGTAGAT
GGGAGACAAGAGGAGATTCCCTGTGGTCATCGCTGCATNTGAAGACAGGCTTGGGGGGGCCAT
TGCAGCTATAAACAGCATTTCAGCACAACACTCGNTCCAATGTGATTTTCTACATTGTTACTC
TCAACAATACAGCAGACCATNTCCGGTCCTGGNTCAACAGTGATTCCCTGAAAAGCATCAGA
TACAAAATTGTCAATTTTGACCCTAAACTTTTGGAAGGAAAAGTAAAGGAGGATCCTGACCA
GGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTCTGGTTCCCAGCG
CAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTTGCCCTTTAC
AATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTCAGCCTCTAC
TAAAGTTGTCATCCGTGGAGCAGGAAA

FIGURE 107

CGACGCTCTAGCGTTACCGCTGCGGGCTGGCTGGGCGTAGTGGGGCTGCGCGGCTGCCACG
 GAGCTAGAGGGCAAGTGTGCTCGGCCAGCGTGCAGGGAACGCGGGCGGCCAGACAACGGGC
 TGGGCTCCGGGGCTGCGGGCGGGCGCTGAGCTGGCAGGGCGGGTCCGGGCGCGGGCTGCA
 TCCGCATCTCTCCATCGCCTGCAGTAAGGGCGGCCGCGCGGAGCCTTTGAGGGGAACGACT
 TGTGAGGCCCTAACCGGGGTGTCTCTGAGCCTGGTGGGATCCCCGGAGCGTCACATCACT
 TTCCGATCACTTCAAAGTGGTTAAAACTAATATTTATATGACAGAAGAAAAAGATGTCATT
 CCGTAAAGTAAACATCATCTTGGTCTGGGCTGTTGCTCTCTTCTTACTGGTTTTGTCAC
 CATAACTTCTCAGCTTGAGGCAGTTTGTAAAGGAATGAGGTTACAGATTGAGGAATTGTAG
 GGCCTCAACCTATAGGACTTTGTCCAAATGCTCTCCGACATGCAGTAGATGGGAGACAAGA
 GGAGATTCTGTGGTCATCGCTGCATCTGAAGACAGGCTTGGGGGGCCATTGCAGCTATAA
 ACAGCATTCAGCACAACACTCGCTCCAATGTGATTTTCTACATTGTTACTCTCAACATACA
 GCAGACCATCTCCGGTCTGGGCTCAACAGTGATTCCCTGAAAAGCATCAGATACAAAATTG
 TCAATTTTGACCTTAACTTTTGAAGGAAAAGTAAAGGAGGATCCTGACCAGGGGGAATCC
 ATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTCTGGGTTCCAGCGCAAAGAAGG
 CCAATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTGCCCTTTACAATACAGCA
 CTGAAGCCAGGACATGCAGCTGCATTTTCAAGATTGTGATTGAGCCTCTACTAAAGTTGT
 CATCCGTGGAGCAGGAACCAAGTACAATTACATTGGCTATCTTGACTATAAAAAGGAAAGAA
 TTCGTAAGCTTTCATGAAAGCCAGCACTTGCTCATTTAATCTGGAGTTTTTGTGCAAAC
 CTGACGGAATGAAACGACAGAATATAACTAACCAACTGGAATAATGGATGAAACTCAATGT
 AGAAGAGGGACTGTATAGCAGAACCCTGGCTGGTAGCATCACAACACCTCCTCTGCTTATCG
 TATTTTATCAACAGCACTCTACCATCGATCCTATGTGGAATGTCCGCCACCTTGGTTCCAGT
 GCTGGAACACGATATTACCTCAGTTTGTAAAGGCTGCCAAGTTACTCCATTGGAATGGACA
 TTTGAAGCCATGGGGAAGGACTGCTTCATATACTGATGTTTGGGGAATAATGGTATATTCCA
 GACCAACAGGCAAATTCAACCTAATCCGAAGATATACCGAGATCTCAAACATAAAGTGAA
 CAGAATTTGAACTGTAAGCAAGCATTTCTCAGGAAGTCTGGAAGATAGCATGCGTGGGAAG
 TAACAGTTGCTAGGCTTCAATGCCTATCGGTAGCAAGCCATGGAATAAGATGTGTGACGCTAG
 GTAAGATGACAACTGCCTGTCTGGCAGTCAGCTTCCAGACAGACTATAGACTATAAAT
 ATGTCTCCATCTGCCTTACCAAGTGTCTTCTTACTACAATGCTGAATGACTGGAAGAAGAA
 CTGATATGGCTAGTTGAGCTAGCTGGTACAGATAATTCAAACCTGCTGTTGGTTTTAATTTT
 GTAACCTGTGGCTGATCTGTAATAAACTTACATTTTTCAATAGGTAAAAAAAAAAAAA
 AAAAAA

FIGURE 108

CTGCAGGTAGACATCTCCACTGCCCAGGAATCACTGAGCGTGCAGACAGCACAGCCTCCTCT
GAAGGCCGGCCATACCAGAGTCCTGCCTCGGCATGGGCCTCACCATTGAGGCAGCTCCACTG
TCTGTGCTGGTCTGAGGGTGTGCTGCTGT**CATG**GGGGCAGCCATCTCCCAGGGGGCCCTCATC
GCCATCGTCTGCAACGGTCTCGTGGGCTTCTTGCTGCTGCTGCTCTGGGTCATCCTCTGCTG
GGCCTGCCATTCTCGTCTGCCGACGTTGACTCTCTCTCTGAATCCAGTCCCAACTCCAGCCC
TGGCCCTGTCTGAGAAGGCCCCACCACCCAGAAGCCCAGCCATGAAGGCAGCTACCTGC
TGCAGCCCTGAAGGCCCTGGCCTAGCCTGGAGCCCAGGACC**TAA**GTCCACCTCACCTAGAG
CCTGGAATTAGGATCCCAGAGTTCAAGCCAGCCTGGGGTCCAGAAGTCAAGAGTCCGCTGCT
TGGAGCTGGACCCAGCGGCCCAGAGTCTAGCCAGCTTGGCTCCAATAGGAGCTCAGTGGCCC
TAAGGAGATGGCCTGGGGTGGGGGCTTATGAGTTGGTGTCTAGAGCCAGGGCCATCTGGACT
ATGCTCCATCCCAAGGGCCAAGGGTCAGGGGCCGGGTCCACTCTTCCCTAGGCTGAGCACC
TCTAGGCCCTCTAGGTTGGGAAGCAAAGTGAACCCATGGCAATAATAGGAGGGTGTCCAG
GCTGGGCCCTCCCCTGGTCTCCAGTGTTTGTGATAATAAATGGAAGTATGGCTCTAA
AAAAAAAAAAAAAAAAA

MGAAISQGALIAIVCNGLVGFLLLLWVILCWACHSRLPTLTLSLNPVPTPALAPVLRPHH
PRSPAMKAATCCSPEGWPSPLEPRT

FIGURE 110

GTTGAATTCCCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGCTACCA
 GTTCCTCCAAGCAAGTCATTTCCCTTATTTAACCGATGTGTCCCTCAAACACCTGAGTGCTA
 CTCCCTATTTGCCATCTGTTTTGATAAATGATGTTGACACCTCCACCGAATTCGAAGTGGAA
 TC**ATG**TCGGGAAGAGATACAATCCTTGGCCTGTGTATCCTCGCATTAGCCTTGCTTTGGCC
 ATGATGTTTTACCTTCAGATTATCACCACCCTTCTGGTTCACATTTTCATTTATTGGTTAT
 TTTGGGATTGTTGTTTGCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACC
 TCAGCATAGAATTGGACACAGAAAGGAAAAATATGAAGTGCCTGCTGGGGTTTGCTATCGTA
 TCCACAGGCATCACGGCAGTGTCTGCTCTTGATTTTTTGTTCTCAGAAAGAGAATAAAATT
 GACAGTTGAGCTTTTCCAAATCACAAATAAGCCATCAGCAGTGTCTCCCTTCTGCTGTTCC
 AGCCACTGTGGACATTTGCCATCCTCATTTTCTCTGGGTCTCTGGGTGGCTGTGCTGCTG
 AGCCTGGGAAGTGCAGGAGCTGCCCAGGTTATGGAAGGCGCCAAAGTGAATATAAGCCCCCT
 TTCGGGCATTTCGGTACATGTGGTCTGACCATTTAATTGGCCTCATCTGGACTAGTGAATTCA
 TCCTTGCGTGCCAGCAAATGACTATAGCTGGGGCAGTGGTTACTTGTATTTCAACAGAAGT
 AAAAATGATCCTCTGATCATCCCATCCTTTCTGCTCTCTCCATTCTCTTCTTCTACCATCA
 AGGAACCGTTGTGAAGGGTCATTTTTAATCTCTGTGGTGAGGATTCCGAGAATCATTGTCA
 TGTACATGCAAAACGCACTGAAAGAACAGCAGCATGGTGCATTGTCCAGGTACCTGTTCCGA
 TGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTCAACCAGAATGCATA
 TACTACAAC TGCTATTAATGGGACAGATTTCTGTACATCAGCAAAAGATGCATTCAAATCT
 TGTCCAAGAACTCAAGTCACTTTACATCTATTAAGTCTTTGGAGACTTCATAATTTTCTA
 GGAAAGGTGTAGTGGTGTGTTTCACTGTTTTTGAGGAGACTATGGCTTTTAAGTACAATCG
 GGCATTCCAGGTGTGGGAGTCCCTCTGTTATTGGTAGCTTTTTTTGCTACTTAGTAGCCC
 ATAGTTTTTTTATCTGTGTTTGAAAGTGTGCTGGATGCACTTTTCTGTGTTTTGCTGTTGAT
 CTGGAAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAAATTTCTGAGTTT
 CGTAAAAGGAGCAACAAATTAACAATGAAGGGCACAGCAGGACAAGCACTCATTAAAGGA
 ATGAGGAGGGAACAGAAGTCCAGGCCATTGTGAGAT**TAG**ATACCATTTAGGTATCTGTACCT
 GGAAAACATTTCTTCTAAGAGCCATTTACAGAATAGAAGATGAGACCCTAGAGAAAAGTT
 AGTGAATTTTTTTTTTAAAGACCTAATAAACCTTATTCTTCTCTCAAA

FIGURE 111

MSGRDTILGLCILALSLAMMFTFRFITTLVHIFISLVILGLLFVCGVLWWLYDYTNDL
SIELDTERENMKCVLGFAIVSTGITAVLLVLIFVLRKRIKLTVELFQITNKAISSAPFLLFQ
PLWTFAILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFI
LACQQMTIAGAVVTCYFNRSKNDPPDHPILSSLSILFFYHQGTVVKGSEFLISVVRIPIIWM
YMQNALKEQQHGALSRYLFRCCYCCFWCLDKYLLHLNQAYTTTAINGTDFCTSAKDAFKIL
SKNSSHFTSINCFGDFIIFLGKVLVVCFTVFGGLMAFYNNRAFAQVWAVPLLLVAFFAYLVAH
SFLSVFETVLDALFLCFAVDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRN
EEGTELQAIVR

FIGURE 112

GTTCGATTAGCTCCTCTGAGAAGAAGAGAAAAGGTTCTTGGACCTCTCCCTGTTTCTTCCTT
 AGAATAATTTGATGGGATTTGTGATGCAGGAAAGCCTAAGGGAAGAAAGATATTCATTCTG
 TGTGGGTGAAAATTTTGTGAAAAAAAATTCCTTCTTCAAACAAGGGTGTCATTCTGATATT
TATCGAGGACTGTGTTCTCACTATGAAGGCATCTGTTATTGAAATGTTCTCTGTTTGTCTGG
TGACTGGAGTACATTCAAACAAGAAACCGGCAAGAAGATTTAAAGGCCCAAGTTCACTGTG
CCCTCAGATCAACTCGGATGCTCAAAGCCGGAAGATCATCGATCCTGAGTTCATTGTGAAATG
TCCAGCAGGATGCCAGAGCCCAATACCATGTTTATGGCACTGAGCTGTATGCATCCTACT
CCAGTCTGTGTGGGCTGCCGTACACAGTGGTGTGCTTGATTAATTCAGGAGGGAATACTT
GTTCCGAAGGTTGCTGGACAGTCTGGTTACAAAGGGAGTTATTCCAACGGTGTCGAATCGTT
ATCCCTACCAGCATGGAGAAATCCTTTATCGTCTTAGAAAAGTAAACCCAAAAAGGGTGTA
CCTACCCTACAGTCTTACATACTCATCATCGAAAAGTCCAGCTGCCCAAGCAGGTGAGACC
ACAAAAGCCTATCAGAGGCCACCTATTCCAGGGACAACCTGCACAGCCGGTCACCTCTGATGCA
GCTTCTGGCTGTCACTGTAGCTGTGGCCACCCCAACCTTGCCAAAGGCCATCCCCTTCTG
CTGCTTCTACCAACAGCATCCCCAGACCACATCAGTGGGCCACAGAGGCCAGGAGATGGAT
CTCTGGTCCACTGCCACCTACACAAGCAGCCAAAACAGGCCAGAGCTGATCCAGGTATCCA
AAGGCAAGATCCTTCAGGAGTGCCTTCCAGAAACCTGTTGGAGCGGATGTCAGCCTGGGAC
TTGTTCCAAAAGAAGAAATTGAGCACACAGTCTTTGGAGCCAGTATCCCTGGGAGATCCAAAC
TGCAAAATTGACTTGTCTGTTTTAATTGATGGGAGCACCAGCATTTGCCAAACGGCGATCCCG
AATCCAGAAGCAGCTCCTGGCTGATGTTGCCCAAGCTCTTGACATTGGCCCTGCCCGTCCAC
TGATGGGTGTGTGCTCAGTATGGAGACAACCTTGCTACTCACTTTAACTTCAAGACACACAG
AAATTCCTGAGATCTGAAGACAGCCATAGAGAAAAATTACTCAGAGAGGAGGACTTTCTAATGT
AGGTCCGGCCATCTCCTTTGTGACCAAGAACTTCTTTCCAAAGCCAAATGGAAACAGAGCGG
GGCTCCCAATGTTGGTGGTGATGGTGGATGGCTGGCCACGGGACAAAGTGGAGAGGCT
TCAGAGATTTGCAGAGAGTCAGGAATCAACATTTTCTTCATCACCATTGAAGGTGCTGCTGA
AAATGAGAAGCAGTATGTGGTGGAGCCCAACTTTGCAAAACAGGCCGCTGTGAGAACAAACG
GCTTCTACTCGCTCCAGGTGCAGAGCTGGTTTGGCCTCCCAAGACCCCTGCAGCCTCTGGTG
AAGCGGGTCTGCGACACTGACCGCTGGCCTGGCAGCAAGACGCTGTTGAACTCGGCTGACAT
TGGCTTCGTCTACGACGGTCCAGCAGTGTGGGGACGGGCACTTCCGCACCGTCTCTCCAGT
CAGTACACCTACGAACAGCGGGCTGGAGTTTGGGTTTCGACAAAGTACAGCAGCAAGCCTGACAT
CCTCAACGCCATCAAGAGGGTGGGCTACTGGAGTGGTGGCACCAGCAGCGGGGCTGCCATCA
ACTTCGCCCTTGAGCAGCTCTTCAAGAAGTCCAAGCCCCAACAGAGGAAGTTAATGATCCTC
ATCACCAGCGGGAGGTCCTACGACGACGTCCGGATCCCAAGCCATGGCTGCCCATCTGAAGGG
AGTGATCACTTATGCGATAGCGGTTGCCTGGGCTGCCCAAGAGGAGCTAGAAGTCATTGCCA
CTCACCCGCCAGAGACCACTCCTTCTTTGTGACAGGTTTGACAACCTCCATCAGTATGTC
CCAGGATCATCCAGAACATTTGTACAGAGTTCAACTCACAGCCTCGGAACTGA**ATTACAGAG**
CAGGCAGAGCACCAGCAAGTGTGCTTTACTAAGTACAGTGTGTGGACACCCCAACCGCTTAA
TGGGGCAGCAGCGGTGCATCAAGTCTTTGGGCAGGGCATGGAGAAACAAATGCTTGTGTTATTA
TTCTCTTGGCATCTCTTTTTCATATTCCAAAACCTTGGAGTTACAAAGATGATCAACAACGT
ATAGAATGAGCCAAAAGGCTACATCATGTTGAGGGTGTGAGAGATTTTACATTTTGACAATT
GTTTCTAAAAATAAATGTTGGGAATACAGTGCAGCCCTTACGACAGGCTTACGTAGAGCTTTT
GTGAGATTTTTAAGTTGTTATTTCTGATTTGAACCTCTGTAACCTCAGCAAGTTTCATTTTT
GTCACTGACAATTAGGAATTTGCTGAATTAATGTTTAGAAGGATGAAAAATAAAAA
AAA
AAA

09990427-111401

FIGURE 113

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKC
 PAGCQDPKYHVYGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYNSGVQSL
 SLPRWRESFIVLESKPKKGVTYPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQPVTLMQ
 LLAVTVAVATPTTLPRPSPSAASTTIPRPQSVGHRSEQEMDLWSTATYTSSQNRPRADPGIQ
 RQDPGGAFFQKPVGADVSLGLVPKEELSTQSLEPVS LGDPNCKIDLSFLIDGSTSIGKRRFR
 IQKQLLADVAQALDIGPAGPLMGVVQYGDNPATHFNLKTHTNSRDLKTAIEKITQRGGLSNV
 GRAISFVTKNFFSKANGNRSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAE
 NEKQYVVEPNFANKAVCRTNGFYSLHVQSWFGLHKTLPVLRVCDTRLACSKTCLNSADI
 GFVIDGSSSVGTGNFRTVLQFVTNLTKEFEISD TDTRIGAVQYTYEQRLEFGFDKYSSKPD I
 LNAIKRVGYWSGGTSTGAAINFALEQLFKKSKPNKRKLMILITDGRSYDDVRI PAMAAHLKG
 VITYAIGVAWAAQEELEVIATHPARDHSFFVDEFDNLHQYVPRI IQNICTEFNSQPRN

CAGGATGAAC TGGTTGCAGTGGCTGCTGCTGTGCGGGGGCGCTGAGAGGACACGAGCTCTA
TGCCCTTTCCGGCTGCTCATCCGCTCGGCCCTCTGTGCGCGCTGCTGCCCTCAGCACCATTGGT
GCGCCAGGTCCCAGCGCTCCGCGCCAGATCCGCGCCACTACAGTTTTTCTCTGACTCTAAT
TGATGCATCGACACCTTGCTGATTTTGGGGAATGTCTCAGAATCCAAAGAGTGGTGAAG
TGCTCCAGGACAGCGTGGACTTTGATATTGATGTGAACGCCCTCTGTGTTTGAACAAACATT
CGAGTGGTAGGAGGACTCCTGTCTGCTCATCTGCTCTCCAAGAAGGCTGGGGTGGAAGTAGA
GGCTGGATGGCCCTGTTCCGGGCCCTCTCTGAGAAATGGCTGAGGAGCGCGGCCGAAAACCTCC
TCCCAGCCTTTACAGACCCCCACTGGCATGCCATATGGAACAGTGAACCTACTTTCATGGCGTG
AACCAGGAGAGACCCCTGTACCTGTACGCGAGGGATTGGGACCTTCATTGTTGAATTTGC
CACCTTGAGCAGCCTCACTGGTGACCCGGTGTTCGAAGATGTGGCCAGAGTGGCTTTGATGC
GCCTCTGGGAGAGCCGGTCAGATATCGGGCTGGTCGGCAACCACATTGATGTGCTCACTGGC
AAGTGGGTGGCCAGGACGCGAGGCATCGGGGCTGGCTGGACTCTCTAGTATTAATTTGGT
GAAAGGAGCCATCTGCTCAGGATAAGAAGCTCAGTGCCATGTTCCCTAGAGTAACAAAG
CCATCCGGAAC TACACCCGCTTCGATGAGTGGTACTGTGGTTTCAGATGTACAAGGGGACT
GTGTCCATGCCAGTCTTCCAGTCCTTGGAGGCC TACTGGCCTGGTCTTCAGAGCCTCATTGG
AGACATTGACAATGCCATGAGGACCTTCTCAACTACTACACTGTATGGAAGCAGTTTGGGG
GGCTCCCGGAATTCTACAACATTCTCAGGGATACACAGTGGAGAAGCGAGAGGGCTACCCA
CTTCGGCCAGA ACTTATTGAAAGCGCAATGTACCTCTACCGTGCCACGGGGGATCCCACCCT
CCTAGAACTCGGAAGAGATGCTGTGGAATCCATTGAAAAATCAGCAAGGTGGAGTGGGAT
TTGCAACAATCAAAGATCTGCGAGACCACAAGCTGGACAACCGCATGGAGTCGTTCTTCTG
GCCGAGACTGTGAAATACCTCTACCTCCTGTTTGACCCAAACCACTTCATCCACAACAATGG
GTCCACCTTCGACGCGGTGATCACCCCTATGGGGAGTGCATCCTGGGGGCTGGGGGGTACA
TCTTCAACACAGAAGCTCACCCCATCGACCTTGCCGCCCTGCACTGCTGCCAGAGGCTGAAG
GAAGAGCAGTGGGAGGTGGAGGACTTGATGAGGGAATTCTACTCTCTCAAACGGAGCAGGTC
GAAATTTCAGAAAAACACTGTTAGTTCGGGGCCATGGGAACCTCCAGCAAGGCCAGGAACAC
TCTTCTCACCAGAAAACATGACCAGGCAAGGGAGAGGAAGCCTGCCAAACAGAAGGTCCCA
CTTCTCAGCTGCCCCAGTCAGCCCTTCACCTCCAAGTTGGCATTACTGGGACAGGTTTTCCT
AGACTCCTCACTAA CCACCTGATAATTTTTTATTTTATTTTGGAGCTAAACTATAATA
AATTGCTTTTGGCTATCATATAA

MPFRLLIPLGLLCALLPQHHGAPGPDGSAPDPAHYSFSLTLIDALDITLLILGNVSEFQRVVE
VLQDSVDFDIDVNASVFETNIRIVVGGLLSAHLLSKKAGVEVEAGWPCSGPFLRMEEAARKL
LPAFQTPPTGMPYGTVNLLHGVNPGETPVTCAGTGTTFIVEFATLSSLTGDPVFEEDVARVALM
RLWESRSDIGLVGNHIDVITGKWVAQDAGIGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNK
AIRNYTRFDDWYLVQWYKGTVSMVPVQSLEAYWPLGSLIGDIDNAMRTFLNYITVWKQFG
GLPEFYNIPOGYTVEKREGYPLRPELIESAMYLYRATGDPTLLELRDAVESIEKISKVECG
FATIKLDRHDLNDRMESFFLAETQVLYLLFDPTNFIHNGNSFDKAVITPYGECILGAGGY
IFNTEAHPDILALAHCCQRLKEWYELDMREFYSLKRSKSFQANTVSSGPWEPPARPPT
LFSPENHDQAREKRPKQKVPLLSCSPQPTSKALLIGOVFLDSS

AAAGTTACATTTTCTGTGGAACCTCTCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTCT
GGCAGAAAGGAGGGTGCTTCGGAGCCCGCCCTTTCTGAGCTTCTGGGCCGGCTCTAGAACAA
ATTGAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT
GAGATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACCTGAGTCTACCA
AATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCT
ACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGCCTGCCCTCAGAACCCT
TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCAGTGATCGCGCTGGAGA
AACAGTGTACTATTCTGTGCAATACCAGGGGGAGTACGAGAGCCTGTACACGAGCCACATCT
GGATCCCCAGCAGCTGGTGCTCACTCACTGAAGTCTGAGTGTGATGTCACTGATGACATC
ACGGCCACTGTGCCATACAACCTTCTGTGTAGGGCCACATTGGGCTCACAGACCTCAGCCTG
GAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTACCCGACCTGGGATGGAGA
TCACCAAAGATGGCTTCCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTTGAGTTC
CTTGTTGGCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAATGGTGAGGAGTGG
GGGTATTCAGTGCACCTAGAAAACCATGGAGCCAGGGGCTGCATACTGTGTGAAGGCCCAGA
CATTCGTGAAGGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA
GATTAGGCCACTTCCCTGGTATGCGCCTTGTTTGCTTTGTTGGCTTCATGCTGATCCTTGT
GGTCTGCGCACTGTTCTGTGGAATAAGGGCCGGCTGCTCAGTACTCTGTTGCCCCGTGG
TGGTCTCCAGACACCTTGAATAATAACCAATTACCCCAAGAACTTAATCAGCTGCAGAGG
GAGGAGGTGGATGCCTGTGCCACGGCTGTGATGTCTCTGAGGAACCTCCTCAGGGCCGGAT
CTCA**TAG**GTTTGGCGAAGGGCCACAGTGAAGCCGAGAACCTGGTCTGCATGACATGGAAC
ATGAGGGGACAAGTTGTGTTTCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA
GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTTGCTAACAGAACAC
TGACTGAGGCTTAGGGGATGTGACCTCTAGACTGGGGGCTGCCACTTGCTGGCTGAGCAACC
CTGGGAAAAGTGACTTTCATCCCTTCGGTCTTAAGTTTTCTCATCTGTAATGGGGGAATTACC
TACACACCTGCTAAACACACACACAGAGTCTCTCTCTATATATACACAGTACACATAAA
TACACCCAGCACCTTGCAAGGCTAGAGGGAACTGGTGACACTCTACAGTCTGACTGATTGAG
TGTTTCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT
GGCTTGGAGAGCCCACTTCCAGAAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG
TGTGAGTTCACTTCAAGCCCAATGCCGGTGAGAGGGGAATGGCTTAGCGAGCTCTACAGT
AGGTGACCTGGAGGAAGGTACAGCCACACTGAAAATGGGATGTGCATGAACACGGAGGATC
CATGAACTACTGTAAAGTGTGACAGTGTGTGCACACTGCAGACAGCAGGTGAAATGTATGT
GTGCAATGCGAGGAGAATGCAAGAAGTCACTAAGTATGATGATGTTGTTGTGCTCCTTTTTTC
TGTGGTAAAGTACAGAATTACGCAAAATAAAAGGGCCACCTTGCCAAAAGCGGTAAAAAA
AAAAA

FIGURE 117

MQTFTMVLEEIIWTSLEFMWFFYALIPCLLTDEVAILPAPQNLSVLSTNMKHLMLMWSFVIAPGE
TVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECDDTDDITATVPYNLRVRATLGSQTS
SILKHPFNRRNSTILTRPGMEITKDGFLVIELEDLGPQFEFLVAYWRREPGAEEHVKMVRSG
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECEVQGEAIPLVLALFAFVGFMILIV
VVPLFVWKMGRLLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

Important features:**Signal peptide:**

amino acids 1-29

Transmembrane domain:

amino acids 230-255

N-glycosylation sites.

amino acids 40-43 and 134-137

Tissue factor proteins homology.

amino acids 92-119

Integrins alpha chain protein homology.

amino acids 232-262

FIGURE 118

TCCTGCTGATGCACATCTGGGTTTGGCAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT
CCTGGCCGGCTCTAGAACAATTCAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGAAAGAAACAATGTTCTAGG
TCAAACCTGAGTCTACCAAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCT
TTTCATGTGGTTTTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGC
CTGCCCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA
GTGATCGCGCCTGGAGAAACAGTGACTATTCTGTGCAATACCAGGGGGAGTACGAGAGCCT
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGTCTCTGAGTGTG
ATGTCACTGATGACATCACGGCCACTGTGCCATACAACCTTTGTGTGAGGGCCACATTGGGC
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTAC
CCGACCTGGGATGGAGATCACCAAAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG
GGCCCCAGTTTGTAGTTCCTTGTGGCCTANTGGAGGAGGGGCGAACCCTTTCGGCGCAAGGG
GTTNGCGAACCCTTTCGGCCGCTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCCAC
ATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGTTGAT

FIGURE 119

CGGACGCGTGGGCCGCCACCTCCGGAACAAGCC**ATG**GTGGCGGCACGGTGGCAGCGGCGTG
GCTGCTCCTGTGGGTGCGGCCCTGCGCGCAGCAGGAGCAGGACTTCTACGACTTCAAGGCGG
TCAACATCCGGGGCAAAC**TGGTGT**CGTGGAGAAGTACCGCGATCGGTGTCCCTGGTGGTG
AATGTGGCCAGCGAGTGC**GGCTT**CACAGACCAGCACTACCGAGCCCTGCAGCAGCTGCAGCG
AGACCTGGGCCCCCACC**ACTTTA**ACGTGCTCGCCTTCCCTTGC**AACCAGTTT**GGCCAAACAGG
AGCCTGACAGCAACAAGGAGATTGAGAGCTTTGCCCGCCGCACCTACAGTGTCTCATTCCCC
ATGTTTAGCAAGATTGCAGTCACCGGTACTGGTGCCCATCCTGCCTTCAAGTACCTGGCCCA
GACTTCTGGGAAGGAGCCACCTGGA**ACTTCT**GGAAGTACCTAGTAGCCCGAGATGGA**AAAGG**
TGGTAGGGGCTTGGGACCCA**ACTGTGT**CAGTGGAGGAGGT**CAGACCC**AGATCAGAGCGCTC
GTGAGGAAGCTCATCCTACTGAAGCGAGAAGACTT**ATAA**CCACCGCGTCTCCTCCTCCACCA
CCTCATCCCGCCACCTGTGTGGGGCTGACCAATGCAA**ACTCAA**ATGGTGCTTCAAAGGGAG
AGACCCACTGACTCTCCTTCTTTACTCTTATGCCATTGGTCCCATCATTCTTGTGGGGGAA
AAATTCTAGTATTTTGAT**TATTTGA**ATCTTACAGCAACAAATAGGA**ACTCCT**GGCCAATGAG
AGCTCTTGACCA**GTGAAT**CACCAAGCCGATACGAACGTCTTGCCAACAAAATGTGTGGCAAA
TAGAAGTATATCAAGCAATAATCTCCACCCAAGGCTTCTGTAAACTGGGACCAATGATTAC
CTCATAGGGCTGTTGTGAGGATTAGGATGAAATACCTGTGAAAGTGCCTAGGCAGTGCCAGC
CAAATAGGAGGCATTCAATGAACATTTT**TG**CATATAAACCAAAAAATA**AACTTGT**TATCAAT
AAAA**ACTTG**CATCCAACATGAATTTCCAGCCGATGATAATCCAGGCCAAAGGTTTAGTGTGT
GTTATTTCTCTGTATTATTTTCTTCATTACAAAAGAAATGCAAGTTCATTGTAACAATCCA
AACAATACCTCAGGATATAAAATAAAATGAAAGTATCCTCCTCAAAA

120/330

FIGURE 120

MVAATVAAAWLLLWAAACAQQEQDFYDFKAVNIRGKLVSLVKYRGSVSLVNVVASECGFTDQ
HYRALQQQLQRDLGPHHFNVLAFFPCNQFGQQEPDSNKEIESFARRTYSVSFFPMFSKIAVTGTG
AHPAFKYLAQTSGKEPTWNFWKYLVPDGGKVGAWDPTVSVEEVRPQITALVRKLILLKREDL

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FIGURE 121

CGGACCGCTGGGCGGGCCGGGACGCAGGGCAAAGCGAGCC**ATG**GCTGTCTACGTCGGGATGC
 TGCCTCTGGGAGGCTGTGCGCCGGGAGCTCGGGGGTGTGGGGGCCCGGGCCGCTCTCT
 CGGAGTTGGCAGGAAGCCAGGTTGCAGGGTGTCCGCTTCTCAGTTCCAGAGAGGTGGATCG
 CATGGTCTCCACGCCCATCGGAGGCTCAGCTACGTTTCAGGGGTGCACAAAAGCATCTTA
 ACAGCAAGACTGTGGGCCAGTGCTTGGAGACCACAGCACAGAGGGTCCCAGAACGAGAGGCC
 TTGGTCGCTCTCCATGAAGACGTCAGGTTGACCTTTGCCCAACTCAAGGAGGAGGTGGACAA
 AGCTGCTTCTGGCCCTCTGAGCATTGGCCCTCTGCAAAGGTGACCGGGTGGGCATGTGGGGAC
 CTAACCTCTATGCATGGGTGCTCATGCAGTTGGCCACCGCCAGCGGGCATCATTCTGGTG
 TCTGTGAACCCAGCCTACCAAGGCTATGGAAGTGGAGTATGTCTCAAGAAGGTGGGCTGCAA
 GGCCCTTGTGTTCCCCAAGCAATTCAAGACCCAGCAATACTACAACGTCTTGAAGCAGATCT
 GTCCAGAAGTGGAGAATGCCACGCCAGGGGGCTTGAAGAGTCAGAGGCTCCAGATCTGACC
 ACAGTCATCTCGGTGGATGCCCCCTTTGCCGGGACCTGCTCCTGGATGAAGTGGTGGCGGC
 TGGCAGCACACGGCAGCATCTGGACCAGCTCCAATACAACCAGCAGTTCCTGTCTGCCATG
 ACCCATCAACATCCAGTTCACCTCGGGGACAAAGGCAGCCCCAAGGGGGCCACCCCTCTCC
 CACTACAACATTGTCAACAACTCCAACATTTAGGAGAGCGCCTGAAACTGCATGAGAAGAC
 ACCAGAGCAGTTGCGGATGATCTGCCCAACCCCTGTACCATTGCCTGGGTTCGTGGCAG
 GCACAATGATGTGTCTGATGTACGGTGCCACCCCTCATCTGGCCTCTCCATCTTCAATGGC
 AAGAAGGCACTGGAGGCCATCAGCAGAGAGAGAGGCACCTTCTGTATGGTACCCCCACGAT
 GTTCGTGGACATTTGAACCCAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAG
 GTGTATTGCTGGGTCCCCGTGCACCTCCAGAGTTGATCCGAGCCATCAACAAGATAAAT
 ATGAAGGACCTGGTGGTTGCTTATGGAACACAGAGAACAGTCCCCTGACATTCGCGCACTT
 CCCTGAGGACACTGTGGAGCAGAAGGCAGAAAGCGTGGGCAGAAATATGCTCTCACACGGAGG
 CCCGGATCATGAACATGGAGGCAGGGACGCTGGCAAAGCTGAACACGCCCGGGGAGCTGTGC
 ATCCGAGGGTACTGCGTCATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGT
 GGATCAGGACAAGTGGTATTGGACAGGAGATGTGCCACAATGAATGAGCAGGGCTTCTGCA
 AGATCGTGGGCGCTCTAAGGATATGATCATCCGGGGTGGTGAGAACATCATCCCCGAGAG
 CTCGAGGACTTCTTTCACACACACCCGAAGGTGACGGAAGTGCAGGTGGTGGGAGTGAAGGA
 CGATCGGATGGGGGAAGAGATTGTGCTTGCATTGCGCTGAAGGACGGGGAGGAGACCAAGG
 TGGAGGAGATAAAAGCTTTCTGCAAAGGGAAGATCTCTACATTCAAGATTCCGAAGTACATC
 GTGTTTGTCAAACTACCCCTCACCATTTCAGGAAAGATCCAGAAATTCAAACTTCGAGA
 GCAGATGGAACGACATCTAAATCTGTGAATAAAGCAGCAGGCTGCTTGGCCGGTTGGCTT
 GACTCTCTCTGTGAGAATGCAACCTGGCTTTATGCACCTAGATGTCCCCAGCACCCAGTTC
 TGAGCCAGGCATCAAAATGTCAAGGAATTGACTGAACGAACTAAGAGCTCCTGGATGGGTC
 CGGGAAGTCGCTGGGCACAAGGTGCCAAAAGGCAGGCCTGCCAGGCCCTCCCTCTCTG
 TCCATCCCCACATTCCTCTGTCTGTCTTGTGATTTGGCATAAAGAGCTTCTGTTTTCTTT
 GAAAAAAAAAAAAAAAAA

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FIGURE 122

MAVYVGMRLRLGRLCAGSSGVLGARAALSRSWQEARLQGVRFLLSSREVD RMVSTPIGGLSYVQ
 GCTPKKHLNSKTVGQCLETTAQRVPEREALVVLHEDVRLTFAQLKEEVDKAASGLLSIGLCKG
 DRLGMWGFNSYAWVLMQLATAQAGIILVSVNPAYQAMELEYVLKKVGCKALVFPKQFKTQQY
 YNVLKQICPEVENAQPGALKSQRLPDLTTVISVDAPLP GTLLLDVVAAGSTRQHLDQLQYN
 QQFLSCHDPINIQTSGTTGSPKGATLSHYNIVNNSNILGERLKLHEKTPEQLRMILPNPLY
 HCLGSVAGTMMCLMYGATLILASPIFNGKKALEAISRERGTFLYGTPTMFVDILNQPDFSSY
 DISTMCGGVIAGSPAPPELIRAIINKINMKDLVVAYGTTENSPVTF AHFPEDTVEQKAESVG
 RIMPHTEARIMMEAGTLAKLNTPGELCIRGYCVMLGYWGEPQKTEEAVDQDKWYWTGDVAT
 MNEQGFCIKIVGRSKDMIIRGGENIYPAELEDFFHTHPKVQEVQVVGKDDRMGEEICACIRL
 KDGEETTVEEIKAFCKGKISHFKIPKYIVFVTNYPLTISGKIQKFKLREQMERHLNL

Signal Peptide:

amino acids 1-22

Transmembrane Domains:

amino acids 140-161, 213-229, 312-334

Putative AMP-binding Domain Signature:

amino acids 260-271

N-myristoylation Sites:

amino acids 19-24, 22-27, 120-125, 203-208, 268-273, 272-277,
 314-319, 318-323, 379-384, 380-385, 409-413

N-glycosylation Site:

amino acids 282-285

FIGURE 123

CAACTCCAACATTTTAGGAGAGCGCCTGAAACTGCATGAGAAGACACCAGAGCAGTTGCGGA
TGATCCTGCCCCAACCCCTGTACCATTGCCTGGGTTCCGTGGCAGGCACAATGATGTGTCTG
ATGTACGGTGCCACCCTCATCCTGGCCTCTCCCATCTTCAATGGCAAGAAGGCACCTGGAGGC
CATCAGCAGAGAGAGAGGCACCTTCCTGTATGGTACCCCCACGATGTTTCGTGGACATTCTGA
ACCAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAGGTGTCATTGCTGGGTCC
CCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAATATGAAGGACCTGGTGGT
TGCTTATGGAACCACAGAGAACAGTCCCGTGACATTCGCGCACTTCCCTGAGGACACTGTGG
AGCAGAAGGCAGAAAGCGTGGGCAGAATTATGCCTCACACGGAGGCGGGGATCATGAACATG
GAGGCAGGGACGCTGGCAAAGCTGAACACGCCCGGGGAGCTGTGCATCCGAGGGTACTGCGT
CATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGTGGATCAGGACAAGTGGT
ATTGGACAGGAGATGTCGCCAC

GAGCAGGACGGAGGCC**ATG**GACCCCGCCAGGAAAGCAGGTGCCCAGGCCATGATCTGGACTGC
AGGCTGGCTGCTGCTGCTGCTGCTTTCGCGGAGGAGCGCAGGCCCTGGAGTGCTACAGCTGCG
TGCAGAAAGCAGATGACGGATGCTCCCCGAACAAGATGAAGACAGTGAAGTGCGCGCCGGGC
GTGGACGCTCTGCACCGAGGCCGTGGGGCGGTGGAGACCATCCACGGACAATTCTCGCTGGC
AGTGCGGGGTTCGCGTTCGGGACTCCCCGGCAAGAATGACCGCGCCCTGGATCTTACGGGC
TTCTGGCGTTTCATCCAGCTGCAGCAATGCGCTCAGGATCGCTGCAACGCCAAGCTCAACCTC
ACCTCGCGGGCGCTCGACCCGGCAGGTAATGAGAGTGATACCCGCCAACGGCTGGAGTG
CTACAGCTGTGTGGGCTGAGCCGGGAGGCGTGCCAGGGTACATCGCCGCCGGTCGTGAGCT
GCTACAACGCCAGCGATCATGTCTACAAGGGCTGCTTCGACGGCAACGCTACCTTGACGGCA
GCTAATGTGACTGTGTCTTGCCTGTCCGGGGCTGTGTCCAGGATGAATTCTGCACTCGGGA
TGGAGTAACAGGCCACAGGTTTCACGCTCAAGTGGCTCTGTGTGCCAGGGGTCCCGCTGTAAC
TGACTCTCGCAACACAGCTACTTCTCCTCTCGAATCCCAACCCCTTGTCCGGCTGCCCTCT
CCAGAGCCCACGACTGTGGCTCAACACACATCTGTACCACTTCTACCTCGGCCCGAGTGAG
ACCCACATCCACCACCAAAACCATGCCAGCGCCAACCAAGTCAGACTCCGAGACGGAGTAG
AACACGAGGCCTCCCGGGATGAGGAGCCCAGGTTGACTGGAGGCGCCGCTGGCCACCAGGAG
CGCAGCAATTGAGGCGAGTATCTGCAAAAGGGGGGCCCCAGCAGCCCCATAATAAAGGCTG
TGTGGCTCCACAGCTGGATTGGCAGCCCTTCTGTGTGGCCGTGGCTGCTGGTGTCTACTGT**T**
GAGCTTCTCCACCTGGAAATTTCCCTCTCACCTACTTCTCTGGCCCTGGGTACCCCTCTTCT
CATCACTTCTCTGTTCCACCAGCTGGACTGGGCTGGCCAGCCCTGTTTTTCAACATTCCC
CAGTATACCCAGCTTCTGCTGCGCTGGTTTTCGCGCTTTGGGAAATAAAATACCGTTGTATAT
ATTCTGCCAGGGGTGTCTAGCTTTTTGAGGACAGCTCCTGTATCCTTCTCATCCTTGTCTC
TCCGCTTGTCTCTTGTGATGTTAGGACAGAGTGAGAGAAGTCAGCTGTACGGGGAAGGTG
AGAGAGAGGATGCTAAGCTTCCTACTCACTTTCTCCTAGCCAGCCTGGACTTTGGAGCGTGG
GGTGGGTGGGACAATGGCTCCCCACTTAAGCACTGCCTCCCTACTCCCGCATCTTTGGG
GATTCGGTTCCCATATGTTCTTCTTACTAGACTGTGAGCTCCTCGAGGGGGGGCCCCGGTAC
CCAATTCGCCCTATAGTGAGTCGTA

FIGURE 125

MDPARKAGAQAMIWTAGWLLLLLLRGGAQALECYSCVQKADDGCS PNKMKTVKCAPGVDVCT
EAVGAVETIHGQFSLAVRGC GSGLP GKND RGLDLHGLLAFIQLQQCAQDRCAKLNLT SRAL
DPAGNESAYPPNGVECYSCVGLSREACQGTSPVVSCYNASDHVYKGC FDGNVTLTAANVTV
SLPVRGCVQDEFCTR DGVTGPGFTLSGSCCQGSRCNSDLRNKTYFSRIPPLVRLPPPEPTT
VASTTSVTTST SAPVRPTSTTKMPAPT SQTPROQVEHEASRDEEPRLTGGAAGHQDRSNSG
QYPAKGGPQQPHNKGCVAPTAGLAALLLAVAAGVLL

[illegible]

FIGURE 127

MELVLVFLCSLLAPMVLASAAEKEKEMDPFHYDYQTLRIGGLVFAVVLFSVGILLILSRCK
CSFNQKPRAPGDEEAQVENLITANATEPQKQRTVEQPSGGSLWNLRRLLEPLDANVDA

099034660

FIGURE 128

AAACTTGAAGCCATGCAGATCCCGGTCTTCTCTGCCGTGGTGCTCCTCTCCCTCCTGGTGCT
CCACTCTGCCCAGGGAGGCCACCTGGGTGGTCTCTGAGGAAGAAAGCACCATTTGAGAATTATG
CGTCACGACCCGAGGCCTTTAAACCCCCGTTCTCTGAAACATCGACAAATTGCGATCTGCGTTT
AAGGCTGATGAGTTCTCGAACTGGCAGCCCTCTTTGAGTCTATCAAAGGAAACTTCCTTT
CTCAACTGTTGGGATGCCTTTCCTAAGCTGAAAGGACTGAGGAGCGCAACTCCTGATGCCAGT
GACCATGACCTCCACTGGAAGAGGGGCTAGCGTGGAGCGTGATTCTCAACCTACCATAACT
CTTTCTCGCTCCAGGAATCAATAAAACATTTTCATCTCAA

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FIGURE 129

MKIPVLPVAVLLSLLVLHSAQGATLGGPEEESTIENYASRPEAFNTPFLNIDKLRSFAKDE
FLNWHALFESIKRKLPFLNWDAFPKLKGLRSATPDAQ

0390427-211401

FIGURE 130

CAGTTCTGAAATCAATGGAGTTAATTTAGGGAATACAAACCAGCCATGGGGGTGGAGATTGC
CTTTGCCTCAGTGATTCTCACCTGCCTCTCCCTTCTGGCAGCAGGAGTCTCCAGGTTGTTT
TTCTCCAGCCAGTTCCAACTCAGGAGACAGGTCCCAAGGCCATGGGAGATCTCTCCTGTGGC
TTTGCCGGCCACTCATGAGAGTGTTTTTGTGTAAGTATTTTTAGAATACTGTTGACTTCT
TCATGATTTAATAACCATCCTTTGCGAAGTTTTATGAGGCTTTAGGGGAATGTCAACCCTCA
AATTTTTGTTATACTAGATGGCTTCCATTTACCCACCCTATTTTAAGGTCCCTTTATTTTT
AGGTTCAAGGTTCAATTTGACTTGAGAAAGTGCCCTTCTGCAGCTTCATTGATTTGTTTATC
TTCACATATTAATTGTAACGATTAATAAAGAATAAGAGCACGCAGACCTCTAGGAGAATATTT
TATCCCTGGGTGCCCTGACACATTTATGTAGTGATCCACAAATGTGATTGTTAATTTAAA
TGTTATTCTAATATTAGTACATTCAAGTTGTGATGTAATATGAATAACCAGAATCTATTTCTT
AAAAGTTTTGAGTATATTTTCACTAGATATTTGTATAGAAAGACTGAATAGTGATG

00390427-111031

[illegible]

0800-762-777

[illegible]

FIGURE 132

GGGGAATCTGCAGTAGGTCGCCGGCC**ATG**GAGTGGTGGGCTAGCTCGCCGCTTCGGCTCTG
 GCTGCTGTTGTTCTCTCCTGCCCTCAGCGCAGGGCCGCCAGAAGGAGTCAGGTTCAAATGGA
 AAGTATTTATTGACCAAAATTAACAGGTCCTTTGGAGAATTACGAACCATGTTCAAGTCAAAAC
 TGCAGCTGCTACCATGGTGTCTAGAGAAGAGGATCTAACTCCTTTCCGAGGAGGCATCTCCAG
 GAAGATGATGGCAGAGGTAGTCAGACGGAAGCTAGGGACCCACTATCAGATCACTAAGAACA
 GACTGTACCGGAAAAATGACTGCATGTTCCCTCAAGGTGTAGTGGTGTGAGCACITTTATT
 TTGGAAGTGATCGGGCGTCTCCCTGACATGGAGATGGTGATCAATGTACGAGATTATCCTCA
 GGTTCTTAAATGGATGGAGCCTGCCATCCCAGTCTTCTCCTTCAGTAAGACATCAGAGTACC
 ATGATATCATGTATCCTGCTTGGACATTTTGGGAAGGGGGACCTGCTGTTTGGCCAATTTAT
 CCTACAGGTCCTGGACGGTGGGACCTCTTCAGAGAAGATCTGGTAAGGTCAGCAGCACAGTG
 GCCATGAAAAAAGAAAAATCTACAGCATATTTCCGAGGATCAAGGACAAGTCCAGAACGAG
 ATCCTCTCATTTCTTCTGTCTCGAAAAACCCAAACTTGTTGATGCAGAATACACCAAAAAAC
 CAGGCCCTGGAAATCTATGAAAGATACCTTAGGAAAGCCAGCTGCTAAGGATGTCCATCTTGT
 GGATCACTGCAAAATACAAGTATCTGTTTAATTTTCGAGGCGTAGCTGCAAGTTTCCGGTTTTA
 AACACCTCTTCTGTGTGGCTCACTTGTTTTCCATGTTGGTGATGAGTGGCTAGAATTCTTC
 TATCCACAGCTGAAGCCATGGGTTCACTATATCCAGTCAAAACAGATCTCTCCAATGTCCA
 AGAGCTGTTACAATTTGTAAAAGCAAATGATGATGTAGCTCAAGAGATTGCTGAAAGGGGAA
 GCCAGTTTATTAGGAACCATTTGCAGATGGATGACATCACCTGTTACTGGGAGAACCTCTTG
 AGTGAATACTCTAAATTCCTGTCTTATAATGTAACGAGAAGGAAAGTTATGATCAAATTAT
 TCCCAAAATGTTGAAAACCTGAAC**TAG**TAGTCATCATAGGACCATAGTCCTCTTTGTGGCA
 ACAGATCTCAGATATCCTACGGTGAGAAGCTTACCATAAGCTTGGCTCCTATACCTTGAATA
 TCTGCTATCAAGCCAAATACCTGGTTTTCTTATCATGCTGCACCCAGAGCAACTCTTGAGA
 AAGATTTAAATGTGTCTAATACACTGATATGAAGCAGTTCAACTTTTGGATGAATAAGGA
 CCAGAAATCGTGAGATGTGGATTTTGAACCAACTCTACCTTTTCAATTTCTTAAGACCAATC
 ACAGCTTGTGCCTCAGATCATCCACCTGTGTGAGTCCATCACTGTGAAATTGACTGTGTCCA
 TGTGATGATGCCTTTGTCCCATTATTTGGAGCAGAAAATTCGTCAATTTGGAAGTAGTACAA
 CTCATTGCTGGAATTGTGAAATTAATTCAAGGCGTGATCTCTGTCACTTTATTTTAATGTAGG
 AAACCCCTATGGGGTTTATGAAAAATACTTGGGGATCATTTCTCTGAATGGTCTAAGGAAGCGG
 TAGCCATGCCATGCAATGATGTAGGAGTTCTCTTTTGTAAAACCATAAACTCTGTACTCAG
 GAGGTTTCTATAATGCCACATAGAAAGAGGCCAATTGCATGAGTAATTATTGCAATTGGATT
 TCAGGTTCCCTTTTTGTGCCTTCATGCCCTACTTCTTAATGCCTCTCTAAAGCCAAA

FIGURE 133

MEWWASSPLRLWLLLFLLPSAQGRQKESGSKWKVFIDQINRSLENYEPCCSSQNCSCYHGVIE
EDLTPFRGGISRKMMAEVVRRLGTHYQITKNRLYREND CMFP SRCSGVEHFILEVIGRLPD
MEMVINVRDYPQVPKWMPEAIPVFSFSKTSEYHDIMYPAWTFWEGGPAVWPIYPTGLGRWDL
FREDLVRSAAQWPWKKNSTAYFRGSRTSPERDPLILLSRKNPKLVD AEYTKNQAWKSMKDT
LGKPAAKDVHLVDHCKYKYLNFNFRGVAASFRFKHLFLCGSLVFHVGD EWLEFFYPQLKPWVH
YIPVKTDLSNVQELLQFVKANDDVAQEIAERGSQFIRNHLQMDDITCYWENLLSEYSKFLSY
NVTRRKG YDQIIPKMLKTEL

FIGURE 134

CACCCCTCCATTTCTCGCC**ATG**GCCCCCTGCACTGCTCCTGATCCCTGCTGCCCTCGCCTCTT
 TCATCCTGGCCTTTGGCACCGAGTGGAGTTCTGTGCGCTTTACCTCCCTTCGGCCACTTCTT
 GGAGGGATCCCGGAGTCTGGTGGTCCGGATGCCGCCAGGGATGGCTGGCTGCCCTGCAGGA
 CCGCAGCATCCTTGCCCCCTGGCATGGGATCTGGGGCTCCTGCTTCTATTGTGGGCAGC
 ACAGCCTCATGGCAGCTGAAAGAGTGAAGGCATGGACATCCCGGTACTTTGGGGTCCCTCAG
 AGGTCACTGTATGTGGCCTGCACTGCCCTGGCCTTGCACTGGTGATGCGGTACTGGGAGCC
 CATACCCAAGGCCCTGTGTTGTGGGAGGCTCGGGCTGAGCCATGGGCCACCTGGGTGCCGC
 TCCTCTGCTTTGTGCTCCATGTCTCTCTGGCTCCTCATCTTTAGCATCCTTCTCGTCTTT
 GACTATGCTGAGCTCATGGGCCTCAAACAGGTATACTACCATGTGCTGGGGCTGGGCGAGCC
 TCTGGCCCTGAAGTCTCCCGGGCTCTCAGACTCTTCTCCACCTGCGCCACCCAGTGTGTG
 TGGAGCTGCTGACAGTGTGTGGTGGTGCCTACCCTGGGCACGGACCGTCTCCTCCTTGCT
 TTCCTCCTTACCCCTCTACCTGGGCCTGGCTCACGGGCTTGATCAGCAAGACCTCCGTACCT
 CCGGGCCAGCTACAAAGAAAACCTCCACCTGCTCTCTCGGCCCCAGGATGGGGAGGCAGAGT**G**
GAGGAGCTCACTCTGGTTACAAGCCCTGTTCTTCTCTCCCACTGAATTCTAAATCCTTAAC
 ATCCAGGCCTGGCTGCTTCATGCCAGAGGCCCAAATCCATGGACTGAAGGAGATGCCCTT
 CTACTACTTGAGACTTTATTCTCTGGGTCCAGCTCCATACCTAAATCTGAGTTTTCAGCCA
 CTGAACTCCAAGGTCCACTTCTCACCAGCAAGGAAGAGTGGGGTATGGAAGTCATCTGTCCC
 TTCCTGTTTAGAGCATGACACTCTCCCCCTCAACAGCCTCCTGAGAAGGAAAGGATCTGCC
 CTGACCACCCCCCTGGCACTGTTACTTGCCTCTGCGCCTCAGGGGTCCCCTTCTGCACCGCT
 GGCTTCCACTCCAAGAAGGTGGACCAGGGTCTGCAAGTTCAACGGTCATAGCTGTCCCTCCA
 GGCCCCAACCTTGCTCACCCTCCCGCCCTAGTCTCTGCACCTCCTTAGGCCCTGCCTCT
 GGGCTCAGACCCCAACCTAGTCAAGGGGATTCTCCTGCTCTTAACTCGATGACTTGGGGCTC
 CCTGCTCTCCCGAGGAAGATGCTCTGCAGGAAAATAAAAGTCAGCCTTTTTCTAAAAAAA

FIGURE 135

MAPALLLIPAAALASFILAFGTGVEFVRFSTSLRPLLGIPESGGPDARQGWLAALQDRSILAP
LAWDLGLLLLFVGQHSLSMAAERVKAWTSRYFGVLQRSYVACTALALQLVMRYWEPIPKGPV
LWEARAEPWATWVPLLCFVLHVISWLLIFSILLVFDYAELMGLKQVYYHVLGLGEPLALKSP
RALRLFSHLRHPVCVELLTVLWVVP TLGTDRLLLAFLLTLYLGLAHGLDQQDLRYLRAQLQR
KLHLLSRPQDGEAE

Signal sequence:

amino acids 1-13

Transmembrane domains:

amino acids 58-76, 99-113, 141-159, 203-222

N-myristoylation sites:

amino acids 37-43, 42-48, 229-235

FIGURE 136

CCGAGCACAGGAGATTGCCTGCGTTTAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGA
 AGAAATTGCCAAACCATGTCTTTTTTCTGTTTCAGAGTAGTTTACAAACAGATCTGAGTGT
 TTTAATTAGCATGGAATACAGAAAAACAACAAAACCTTAAGCTTTAATTTCACTCTGGAATT
 CCACAGTTTTTCTTAGCTCCCTGGACCCGGTTGACCTGTTGGCTCTTCCCGCTGGCTGCTCTA
 TCACGTGGTGTCTCCGACTACTACCCCGAGTGTAAGAACCTTCGGCTGCGTGTCTCTG
 AGCTGCTGTGCAATGCGCTCTCTGGACTGTCTTCCGAGTAGGATGTCACTGAGATCC
 CTCAAATGGAGCCTCCTGCTGTGTCACTCCTGAGTTTCTTTGTGATGTGGTACCTCAGCCT
 TCCCCACTACAATGTGATAGAACGCGTGAAGTGGATGTACTTCTATGAGTATGAGCCGATTT
 ACAGACAAGACTTTCACTTTCACACTTCGAGAGCATTCAAACGTCTCTCATCAAATCCATTT
 CTGGTCACTTCTGGTGACCTCCACCCCTTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTAC
 TTGGGTGAAAAAAGTCTTGGTGGGGATATGAGGTTCTTACATTTTCTTATTAGGCCAAG
 AGGCTGAAAAGGAAGACAAAATGTTGGCATTGTCTTAGAGGATGAACACCTTCTTTATGGT
 GACATAATCCGACAAGATTTTTTAGACACATATAATAACCTGACCTTGAAAACCATATGGC
 ATTCAGGTGGGTAAGTGTGTTTTGCCCCAATGCCAAGTACGTAATGAAGACAGACACTGATG
 TTTTCACTCAATACTGGCAATTTAGTGAAGTATCTTTTAAACCTAAACCACTCAGAGAAGTTT
 TTCACAGGTATCTCTAATTGATAATTATTCCTATAGAGGATTTTACAAAAAACCATAT
 TTCTTACCAGGAGTATCTTTCAAGGTGTTCCCTCCATACTGCAGTGGGTTGGGTATATATA
 GTGCCAGAGATTTGGTGCAAGGATCTATGAAATGATGGGTACGTAACCAATCATATTCAGAAGA
 GAAGATGTTTTATGTCGGGATCTGTTTGAATTTATTAAAGTGAACATTCATATTCAGAAGA
 CACAAATCTTTTCTTTCTATATAAGAATCCATTTGGATGTCTGTCAACTGAGACGTGTGATTG
 CAGCCCATGGCTTTTCTTCCAAGGAGATCATCACTTTTGGCAGGTCATGCTAAGGAACACC
 ACATGCCATTATTAACCTTCACATTCTACAAAAAGCCTAGAAGGACAGGATACCTTGTGGAAA
 GTGTAAATAAAGTAGGTACTGTGAAAAATTATGGGGAGGTGAGTGTGCTGGCTTACACTG
 AACTGAAACTCATGAAAAACCCAGACTGGAGACTGGAGGGTTACACTTGTGATTATTAGTC
 AGGCCCTTCAAAGATGATATGTGGAGGAATTAATATAAAGGAATTGGAGGTTTTTGTCTAAA
 GAAATTAATAGGACCAACAATTTGGACATGTCATTCTGTAGACTAGAATTTCTTAAAGGG
 TGTTACTGAGTTATAAGCTCACTAGGCTGTAAAACAAAACAAATGTAGAGTTTTATTATTG
 AACAAATGTAGTCACTTGAAGGTTTTGTGTATATCTTATGTGGATTACCAATTTAAAAATATA
 TGTAGTTCTGTGTCAAAAACTTCTTCACTGAAGTTTACTGAACAAAATTTTACCTGTTTT
 TGGTCAATTTATAAAGTACTTCAAGATGTTGCAGTATTTACAGTTATTATTATTAAAAATTA
 CTTCAACTTTGTGTTTTTAAATGTTTTGACGATTTCAATACAAGATAAAAGGATAGTGAAT
 CATTCTTTACATGCAACATTTTCCAGTTACTTAACTGATCAGTTTATTATTGATACATCAC
 TCCATTAATGTAAAGTCATAGGTCAATTATGTCATATCAGTAATCTCTTGGACTTGTAAAT
 ATTTTACTGTGGTAATATAGAGAAGAAATTAAGCAAGAAAATCTGAAAA

FIGURE 137

MASALWTVLP SRMSLRSLKWSLLLLSLLSFFVMWYLSLPHYNVIERVNWMYFYEYEP IYRQD
FHFTLREHSNC SHQNPFVLVLTSHPSDV KARQAIRVTWGEKKSWWGYEVLTFLLGQEAEK
EDKMLALSLEDEHLLYGDIIRQDFLDTYNNLT LKTIMAFRWVTEFCPNAKYVMKTDTDVFIN
TGNLVKYLLNLNHSEKFFTGYPLIDNYSYRGFYQKTHISYQEYPPKVFPYCSGLGYIMSRD
LVPRIYEMMGHV KPIKFEDVYVGICLNLLKVNIHIPEDTNLFFLYRIHL DVCQLRRVIAAHG
FSSKEIITFWQVMLRNTTCHY

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FIGURE 138

CCTCTGTCCACTGCTTTCGTGAAGACAAG**ATGA**AGTTCACAATTGTCTTTGCTGGACTTCTT
GGAGTCTTTCTAGCTCCTGCCCTAGCTAACTATAATATCAACGTCAATGATGACAACAACAA
TGCTGGAAGTGGGCAGCAGTCAGTGAGTGTCAACAATGAACACAATGTGGCCAATGTTGACA
ATAACAACGGATGGGACTCCTGGAATCCATCTCTGGGATTATGGAAATGGCTTTGCTGCAACC
AGACTCTTTCAAAAGAAGACATGCATTGTGCACAAAATGAACAAGGAAGTCATGCCCTCCAT
TCAATCCCTTGATGCACCTGGTCAAGGAAAAGAAGCTTCAGGGTAAGGGACCAGGAGGACCAC
CTCCCAAGGGCCTGATGTACTCAGTCAACCCAAACAAGTCGATGACCTGAGCAAGTTCGGA
AAAAACATTGCAACATGTGTCGTGGGATTCCAACATACATGGCTGAGGAGATGCAAGAGGC
AAGCCTGTTTTTTTACTCAGGAACGTGCTACACGACCAGTGTAATGATGGATTGTGGACATTT
CCTTCTGTGGAGACACGGTGGAGAACT**TAA**ACAATTTTTTAAAGCCACTATGGATTTAGTCAT
CTGAATATGCTGTGCAGAAAAAATATGGGCTCCAGTGGTTTTTACCATGTCATTCTGAAATT
TTTCTCTACTAGTTATGTTTGATTCTTTAAGTTTCAATAAAATCATTTAGCATTGAAAAAAA

FIGURE 139

MKFTIVFAGLLGVFLAPALANYNINVNDDNNNAGSQQSVSVNNEHNVANVDNNGWDSWNS
IWDYGNNGFAATRLFQKKTCIVHKMNKEVMPSIQSLDALVKEKKLQKGKGGPPPKGLMYSVN
PNKVDDLKFKGNIANMCRGIPTYMAEEMQEASLFFYSGTCYTTSVLWIVDISFCGDTVEN

Signal Peptide:

amino acids 1-20

N-myristoylation Sites:

amino acids 67-72, 118-123, 163-168

Flavodoxin protein homology:

amino acids 156-174



CAATTCTGAAACTAAICGTGTCAGAATTGACTTTGAAAAGCATTGCTTTTTACAGAAGTATA
TTAACTTTTTAGGAGTAATTTCTAGTTTGGATTGTAATATGAAATAATTTAAAGGGCTTCG
CTCATATATAGGAAAATCGCATATGGTCTAGTATTAATTCCTATTGCTTACTGATTTTTT
TGAGTTAAGAGTTGTTATATGCTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAAA
GAATAAAGTAGATTGAGTCTCCAATTTTATGTAGCTTCAGAGAAGCTGGTTTGTTACATG
CAAGCTTATAGTTGAAATATTTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGT
TTGTTTCGATTTCAACCAGAGACTATAGCATGTGCTTGCATCTACCTTGCAGCTAGAGCACTT
CAGATTCGGTTGCCAACTCGTCCCCATTGGTTTCTTCTTTTTGGTACTACAGAAGAGGAAAT
CCAGGAAATCTGCATAGAAAACACTTAGGCTTTATACCAGAAAAAGCCAACTATGAATTAC
TGAAAAAGAAGTAGAAAAAGAAAAGTAGCCTTACAAGAAGCCAAATTTAAAGCAAAGGGA
TTGAATCCGGATGGAAGTCCAGCCCTTTCAACCTGGGTGGATTTTCTCCAGCTCCAAGCC
ATCATACCAAGAGAAGTAAAAGCTGAAGAGAAATACCAATCTTCAATTAATGTGAAGAC
TCAAAAAGGAACCTGAGGATAGACAGACGCTTCCAAAAGCCCTTCAATGTGTGTAAGAAAA
GACAGCAAGAGAAGTAGAAATAGCAGAAGTGCAAGTCGATCGAGGTCAAGAACACGATCAGC
TTCTAGATCACATACTCCAAGAAGACACTATAATAATAGGCGGAGTCGATCTGGAACATACA
GCTCGAGATCAAGAAGCAGGTCCCGCAGTCACAGTGAAGGCCCTCGAAGACATCATAATCAT
GGTTCTCTCACCTTAAGGCCAAGCATACCAGAGATGATTTAAAAAGTTCAAACGAGCATGG
TCATAAAAGGAAAAAATCTCGTTCTCGATCTCAGAGCAAGTCTCGGGATCACTCAGATGCAG
CCAAGAAACACAGGCATGAAAGGGGACATCATAGGGACAGCGTGAACGATCTCGCTCCTTT
GAGAGGTCCCATAAAGCAAGCACCATTGGTGGCAGTCGCTCAGGACATGGCAGGCACAGCGC
CTGACTTTCTCTCTTTGAGCCTGCATCAGTTGTTGGTTTTGCCTATCTACAGTGTGATGT
ATGGAICTCAATCAAAAACATTAAACGCAAACCTGATTAGGATTTGATTTCTTGAAACCCCTCTA
GGTCTCTAGAACACTGAGGACAGTTTCTTTTGAAAAGAACTATGTTAATTTTTTGCACATT
AAAATGCCCTAGCAGTATCTAATTAAAAACCATGGTCAGGTTCAATTGTACTTTATTATAGT
TGTGTATTGTTTATTGCTATAAGAACTGGAGCGTGAATCTGTAAAAATGTATCTTATTTTT
ATACAGATAAAAATTGCAGACACTGTCTATTTAAGTGGTTATTTGTTTAAATGATGGTGAAT
ACTTTCTTAACACTGTTTTGTCTGCATGTGTAAGATTTTTACAAGGAAATAAAATACAAAT
CTTGTTTTTTCTAAAAAAGAAAAAAGT

FIGURE 141

MNDSLRTNVFVRFPETIACACIYLAARALQIPLPTRPHWFLFLFGTTEEEIQEICIETLRLY
TRKKPNYELLEKEVEKRKVALQEAKLKAKGLNPDGTPALSTLGGFSPASKPSSPREVKAEEK
SPI SINVKTVKKEPEDRQQASKSPYNGVRKDSKRSRNSRSASRSRSRTRSRSRSHTPRRHYN
NRRSRSGTYSSRSRSRSRSHSESPRRHHNHGSPHLKAKHTRDDLKSSNRHGHKRKKSRSRSQ
SKSRDHSDAAKKHRHERGHHRDRRERSRSFERSHKS KHHGGSRSRSGHRHRR

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FIGURE 142

TGGGGATAAAGGAAAAATGGTCAGGTATTAATGGCTTAAAGATTATTGGAAGGGGTTTATCA
TTTTTTGAANNATATCGGGTCANAATTGNCTTTGAAAAGCATTGCTTTTTACAGAAATATAT
TANCTTTTtagagTAATTTCTAGTTTGGATTGTAATATGAAATTATTTAAAGGGCTTCGCT
CATATATAGGAAAAATCGCATATGGTCCTAGTATTAAATNTTATTGCTTACTGATTTTTTTG
AGTTAAGAGTTGTTATATGNTAGAATATGAGGATGTGAATATAAAATAAGAGAAGAAAAAAGA
ATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAAGCTGGTTTGTTTACATGCA
AGCTTATAGTTGAAATATTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGTTT
GTTTCGATTTCAACCAGAGANTATAGCATGTGCTTGCATCTACCTTGCAGNTAGAGCACTTCA
GATTCCGTTGCCAACTNGTCCCATTTGGTTTCTTCTTTTGGTACTACAGAAGAGGAAATCC
AGGAAATNTGCATAGAAACACTTAGGCTTTATACCAGAAAAAGCCAACTATGAATTACTG
GAAAAAGAAGTAGAAAAAGAAAAGTAGCCTTACAAGAAGCCNAATTAAAAGCAAAGGGATT
GAATCCGGATGGAAGCTCCAGCCCTTTCAACCCTGGGTGGATTTTCTCC

FIGURE 143

GGACACGAGGCCTCGTGCCAAGCTTGGCACGAGGGTGCACCGCGTTCTCGCACGCGTCATGGCAGGCTCGGAGTACAGCTGGTGGTGACCCGTGCTCACTGCCACCCTCATGCACAGGCTGGCGC
CACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAAACGGCAGTTTGTTCGGATACAAGCACCCG
TCTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCCAGAGGCAGGAAAGAGCGGTG
GGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCGGAGATGCCCGGTTCCAGCTGG
AGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCTGCGCTTCTTCTCGAGTACCAGTGG
TTTGTGGACTTTGCTGTGTACTCGGGCGGCGTGTACCTCTTACAGAGGCCCTACTACTACAT
GCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGTGCTGCTCACGGTGACCTTCT
CCATCAAGATGTTCTGACAGTGACACGGCTGTACTTTCAGCGCCGAGGAGGGGGGTGAGCGC
TCTGTCTGCCTCACCTTTGCCTTCTCTTCTGCTGCTGGCCATGCTGGTGCAAGTGGTGCG
GGAGGAGACCCCTCGAGCTGGGCTGGAGCCTGGTCTGGCCAGCATGACCCAGAACTTAGAGC
CACTTCTGAAGAAGCAGGCTGGGACTGGGCGCTTCTGCTGGCCAAGCTGGCTATCCGCGTG
GGACTGGCAGTAGTGGGCTCTGTGCTGGGTGCCCTTCTCACTTCCCAGGCTGACCGCTGGC
CCAGACCAACCGGGAGCAGCACTGACATGCTCGGAGGACAGACCATGCTGCAAGTTCTCTCTGC
ACACCAGCTTCTGTCTCCCTGTTTCATCTGTGGCTCTGGACAAGGCCATTGCACGGGAC
TTCTTGACACAGCCGCGCTTTGGGGAGACGCGTTTCTCCTGCTGTCCGATTCTGCCTTCGA
CTCTGGGCGCCTCTGGTTGCTGGTGGTGTGCTGCGCTGCTGCGGCTGGCGGTGACCCGGCCCC
ACCTGCAGGCCTACCTGTGCCTGGCCAAGGCCCGGGTGGAGCAGCTGCGAAGGGAGGCTGGC
CGCATCGAAGCCCGTGAAATCCAGCAGAGGGTGGTCCGAGTCTACTGCTATGTGACCGTGGT
GAGCTTGCACTACCTGACGCCGCTCATCTCACCTCAACTGCACACTTCTGCTCAAGACGC
TGGGAGGCTATTCTGGGGCTGGGCGCCAGCTCCTCTACTATCCCCGAGCCATCTCAGCC
AGCGCTGCCCCATCGGCTCTGGGGAGGACGAAGTCCAGCAGACTGCAGCGCGGATTGCCGG
GGCCTGGGTGGCTGCTTACTCCCTCTTCTCCTCGTGCGCTCTGGCCTACCTCATCTGGT
GGACGGCTGCCTGCCAGCTGCTCGCCAGCCTTTTCGGGCTCTACTTCCACCAGCACTTGGCA
GGCTCCCTAGCTGCCTGCAGACCTCTGGGGCCCTGAGGTCTGTTCTGGGGCAGCGGGACA
CTAGCCTGCCCCCTCTGTTTGCGCCCCGCTGTCCCCAGCTGCAAGGTGGGGCCGGACTCCCC
GGCGTTCCCTTACCACAGTGCTGACCCGCGGCCCCCTTGGACGCCGAGTTTCTGCCTCA
GAATGCTTCTCTGGGCCAGCAGCATGAGGGTCCCAGGCCATTGTCTCCGAAGCGTATG
TGCCAGGTTTGTAGTGGCGAGGGTGATGCTGGCTGCTCTTCTGAACAAATAAAGGAGCATGCC
GATTTTAA

FIGURE 144

MAVLGVQLVVTLTATLMHRLAPHCSFARWLLCNGSLFRYKHPSEELRALAGKPRPRGRKE
RWANGLSEEKPLSVPRDAPFQLETCPLTTVDALVLRFFLEYQWFVDFAVYSGGVYLFTEAYY
YMLGPAKETNIAVFWCLLTVTFSIKMFMTVTRLYFSAEEGGERSVCLTFAFLFLLAMLVQV
VREETLELGLPEGLASMTQNLEPLLKKQGDWALPVAKLAIRVGLAVVGSVLGAFLTFPGLR
LAQTHRDALTMSEDRPMLQFLLHTSFLSPLFILWLWTKPIARDFLHQPPFGETRFSLLSDSA
FDSGRLLVVLCLLRLAVTRPHLQAYLCLAKARVEQLRREAGRIEAREIQQRVVRVYCYVT
VVSLLQYLTPLILTLNCTLLLKTLGGYSWGLGPAPLLSPDPSSASAAPIGSGEDEVQQTAARI
AGALGGLLTPLFLRGVLAYLIWWTAACQLLASLFGLYFHQHLA

FIGURE 145

CGTTNGCAGCGTCAATGGCGGTCCTCGGAGTACAGCTGGTGGTGACCCTGCTCACTGCCAC
CCTCATGCACAGGCTGGCGCCACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAAACGGCAGTT
TGTTCCGATACAAGCACCCGTTNTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCC
CAGAGGCAGGAAAGAGCGGTGGGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCC
GAGATGCCCCGTTCCAGCTGGAGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCCTGCGC
TTCTTCCTGGAGTACCAGTGGTTTGTGGACTTTGCTGTGTACTCGGGCGGCGGTGACCTCTT
CACAGAGGCCTACTACTACATGCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGT
GCCTGCTCACAGTGACCTTCTCCATCAAGATGTTTCCTGACAGTGACACGGCTGTACTTCAGC
GCCGAGGAGGGGGGTGAGCGCTCTGTCTGCCTCACCTTGCCTTCCTCTTCCTGCTGCTGGC
CATGCTGGTGCAAGCG

FIGURE 146

GGTTCCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTTACGGGGCCCGTGATTATTAAACGTGGCTT
 AATCTGAAGGTTCTCAGTCAAAATCTTTGTGATCTACTGATTGTGGGGGCATGGCAAGGTTTGCTTAAAGGAGC
 TTGGCTGGTTTGGGCCCCGTGTAGCTGACAGAAGTTGGCCAGGGAATGCAGCACA CTGCTCGGAGAA**TGA**AGG
 CGCTTCTGTTGCTGCTCTTGCCCTGGCTCAGTCTCTGCTAACTACATTGACAATGTGGGCAACCTGCACCTCCTG
 TATTCAAGAATCTGTAAGAGTGCCTCCCACTACGGCTGACCAAGATAGGAAGGGCGCTCACAAGATGGCTG
 TCCAGACGGCTGTGCGAGCTCACAGCCACGGCTCCCTCCCAGAGGTTTCTGCAGCTGCCACCATCTCCTTAA
 TGACAGACGAGCTGGCTAGACAACCTGCTACGTGCTCCTCGGCAGAGGACGGGCAGCCAGCATCAGCCCA
 GTGGACTCTGGCCGGAGCAACCGAATAGGGCAGGGCCCTTTGAGAGATCCACTATTAGAGCAGATCATTAA
 AAAAATAAATCGAGCTTTGAGTGTTCTTGAAGGACAAAGAGCGGGAGTGCACTTGCCAAACCATGCCGACGAG
 GCAGGGAAATCTGAAAACACCACTGCCCTGAAGTCTTTCCAAAGTTGTACCACTGATTCCAGATGGTGAA
 ATTACAGCATCAAGATCAATCGAGTAGATCCCAGTGAAGGCTCTCTATTAGGCTGGTGGGAGGTAGCGAAAC
 CCCACTGGTCCATATCATTATCCAACACATTATCTGTGATGGGGTGATGCCAGAGACGGCCGGCTACTGCCAG
 GAGACATCATTTAAAGTCAACGGGATGGACATCAGCAATGTCCCTCACAACCTACGCTGTGCGTCTCTGCCG
 CAGCCCTGCCAGGTGCTGTGGCTGACTGTGATGCGTGAACAGAAGTTCCGCAGCAGGAACAATGGACAGGCCCC
 GGATGCCACAGACCCCGAGATGACAGCTTTCATGTGATTCTCAACAAAAGTAGCCCCGAGGAGCAGCTTGGA
 TAAACTGGTGGCAAGGTGGATGAGCCTGGGGTTTTCATCTTCAATGTGCTGGATGGCGGTGTGGCATATCGA
 CATGGTCAGCTTGAGGAGATGACCGTGTTAGCCATCAATGGACATGATCTCGATATGGCAGCCAGAAAG
 TCGCGCTCATCTGATTGAGGCCAGTGAAGACGTGTTCACTCGTCTGTGCCGCCAGGTTCCGCAGCGGAGCC
 CTGACATCTTTGAGGAAGCCGGCTGGAACAGCAATGGCAGCTGGTCCCCAGGGCCAGGGGAGAGGAGCAACACT
 CCCAAGCCCCCATCTCAATAATTCTTGTATGAGAAGTGGTAAATATCCAAAAGACCCCGGTGAATCTCT
 CGGCATGACCGTCGCGAGGGGAGCATCACATAGAGAATGGGATTGGCTATCTATGTCTCATGCTGTGAGCCG
 GAGGATCATAAAGCAGAGATGGAAGAATAAAACAGGTGACATTTGTTGAATGGGATGGGGTCGAATGACA
 GAGGTGAGCCGAGTGAGGCACTGGCATTATTGAAAAGAACATCATCTCGATAGTACTCAAAGCTTTGGAAGT
 CAAAGAGTATGAGCCCCAGGAAGACTGCAGCAGCCAGCAGCCCTGGACTCCAAGCAACATGGCCCCACCCA
 GTGACTGGTCCCCATCTGGGTGATGTGGCTGGAATTACCACGGTGCTGTATACTGTAAGATATTGTATTA
 CGAAGAACAACAGCTGGAAGTCTGGGCTTCTGCATTGTAGGAGTTATGAAGAATAAATGGAACAAACCTTT
 TTTTCATCAATCCATGTTGAAGAACACACAGCATACATGATGGAAGATTAGATGTGGTGATATTTCTCTTG
 CTGTCAATGGTAGAATACATCAGGAATGATACATGCTTGGCAAGACTCTGAAAGAACTTAAAGGAAGA
 ATTACTCTAACTATTGTTTCTTGGCTGGCACTTTT**TGAGA**ATCAATGATGGTCAAGGAAAAACAGAAAAA
 TCACAAATAGGCTAAGAGTTGAACACTATATTTATCTTGTCAGTTTATATTTAAAGAAAGAAATACATTGT
 AAAAATGTCAAGAAAGATGATCATCTAATGAAGGCCAGTTACACCTCAGAAAAATGATTTCCAAAAAATTA
 AAACATCTAGTTT**TTTT**TCAGTGTGGAGGATTTCTCATCTCTACACATGTGTATATTTTCTATCTCAAT
 AAAAGCCCTTAAACAACTAAATGATTGATTGTATATCCCACTGAATCAAGCTGATTAAATTTAAATTT
 GGTATGCTGAAGCTGCCAAGGTACATATGGCCATTT**TAATTT**TACAGTAAATATTTTAAATTTGA
 TTGCTGAGAAGCTTGCTTTCATCAACAGAATAAATATTTT**CAGA**AGTTAAA

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FIGURE 147

MKALLLLVLPWLSPANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGC PDGCASLTAT
APSPEVSAAATISLMTDEPGLDNPAYVSSAEDGQPAISPVDSGRSNRTRARPFERSTIRSR
FKKINRALSVLRRTKSGSAVANHADQGRENSSENTAPEVFPRLYHLIPDGEITSIKINRVDP
SESLSIRLVGGSETPLVHIIIQHIYRDGVIARDGRLLPGDIILKVNGMDISNVPHNYAVRLL
RQPCQVLWLTVMREQKFRSRNNGQAPDAYRPRDDS FHVILNKSSPEEQ LGIKLVRKVDEPGV
FIFNVLDGGVAYRHGQLEENDRVLAINGHDLRYGSPESA AHLIQASERRVHLVVS RQVRQRS
PDIFQEAGWNSNGSWSPGPGERSNTPKPLHPTITCHEKVVNIQKDPGESLGMTVAGGASHRE
WDLPIYVISVEPGGVISR DGRIKTGDILLNVDGVELTEVSRSEAVALLKRTSSSIVLKALEV
KEYEPQEDCSSPAALDSNHNMAPPSDWSPSWVMWLELPRCLYNCKDIVLRNTAGSLGFCIV
GGYEEYNGNKPF FIKSIVEGTPAYNDGRI RCGDILLAVNGRSTSGMIHACLARLLKELKGRI
TLTIVSWPGTFL

FIGURE 148

CCAAAGTGATCATTGTGAAAAAGAGATATCCACATCTTCAAGCCCATATAAAGGATAGAAGCT
 GCACAGGGCAGCTTTACTTACTCCAGCACCTTCCTCTCCAGGCCAAATGCTGCTGACCATCT
 TTGGGATACAATCTCATGGATACGAGGTTTTTAACATCATCAGCCCAAGCAACAATGGTGGC
 AATGTTTCAGGAGACAGTGACAATTGATAATGAAAAAATACCGCCATCGTTAACATCCATGC
 AGGATCATGCTCTTCTACCACAATTTTTGACTATAAACATGGCTACATTGCATCCAGGGTGC
 TCTCCCGAAGAGCCTGCTTTATCCTGAAGATGGACCATCAGAACATCCCTCCTCTGAACAAT
 CTCCAATGGTACATCTATGAGAAACAGGCTCTGGACAACATGTTCTCCAACAAATACACCTG
 GGTC AAGTACAACCTCTGGAGTCTCTGATCAAAGACGTGGATTGGTTCCTGCTTGGGTCAC
 CCATTGAGAACTCTGCAAACATATCCCTTTGTATAAGGGGAAGTGGTTGAAAACACACAT
 AATGTCGGTGTCTGGAGGCTGTGCAAAGGCTGGGCTCCTGGGCATCTGGGAATTTCAATCTG
 TGCAGACATT CATGTTTAGGATGATTAGCCCTCTTGTTTTATCTTTTCAAAGAAATACATCC
 TTGGTTTACACTCAAAAGTCAAATTAAATCTTTCCCAATGCCCCAACTAATTTTGAGATTC
 AGTCAGAAAAATATAAATGCTGTATTATA

0099027-14401
 10111-240000

FIGURE 149

MKILVAFLLVLTIFGIQSHGYEVFNIIISPSNNGGNVQETVTIDNEKNTAIVNIHAGSCSSTT
IFDYKHGYIASRVLRRACFILKMDHQNIPLNQLWYIYEKQALDNMFSNKYTWVKYNPLE
SLIKDVDWFLGSPIEKLCKHIPLYKGEVVENTHNVGAGGCAKAGLLGILGISICADIHV

FIGURE 150

GGCACGAGCCAGGAAC TAGGAGGTTCTCACTGCCCCGAGCAGAGGCCCTACACCCACCGAGGC
ATGGGGCTCCCTGGGCTGTTCTGCTTGCCGTGCTGGCTGCCAGCAGCTTCTCCAAGGCACG
GGAGGAAGAAATTACCCCTGTGGTCTCCATTGCCTACAAAGTCTTGGAAGTTTTCCCAAAG
GCCGCTGGGTGCTCATAACCTGCTGTGCACCCAGCCACCACCGCCCATCACCTATTCCCTC
TGTGGAACCAAGAACATCAAGGTGGCCAAGAAGTGGTGAAGACCCACGAGCCGGCCTCCTT
CAACCTCAACGTCACTCAAGTCCAGTCCAGACCTGCTCACCTACTTCTGCCGGGCGTCTT
CCACCTCAGGTGCCCATGTGGACAGTGCCAGGCTACAGATGCACTGGGAGCTGTGGTCCAAG
CCAGTGTCTGAGCTGCGGGCCAACTTCACTCTGCAGGACAGAGGGGAGGCCCCAGGGTGGA
GATGATCTGCCAGGCGTCTCGGGCAGCCACCTATCACCACAGCCTGATCGGGAAGGATG
GGCAGGTCCACCTGCAGCAGAGACCATGCCACAGGCAGCCTGCCAACTTCTCCTTCTGCCG
AGCCAGACATCGGACTGGTTCTGGTGCCAGGCTGCAAACAACGCCAATGTCCAGCACAGCGC
CCTCACAGTGGTGCCCCAGGTGGTGACCAGAAGATGGAGGACTGGCAGGGTCCCCTGGAGA
GCCCATCCTTGCCCTTGCCGCTCTACAGGAGCACCCGCCGTCTGAGTGAAGAGGAGTTGGG
GGGTTCAGGATAGGGAATGGGAGGTGAGAGGACGCAAAGCAGCAGCCATG**TAGA**ATGAACC
GTCCAGAGAGCCAAGCACGGCAGAGGACTGCAGGCCATCAGCGTGCACTGTTCTGATTTGGA
GTTTCATGCAAAATGAGTGTGTTTTAGTGTCTTGCCACAAAAAAAAAAAAAAAAAAAAA

FIGURE 151

MGLPGLFCLAVLAASSFSKAREEEITPVVSIAYKVLEVFPKGRWVLITCCAPQPPPPITYSL
CGTKNIKVAKKVVKTHEPASFNLNVTLKSSPDLLTYFCRASSTSGAHVDSARLQMHWELWSK
PVSELNANFTLQDRGAGPRVEMICQASSGSPPIITNSLIGKDGVHLQQRPCRQPANFSFLP
SQTSDWFWCQAANNANVQHSALTVVPPGGDQKMEDWQGPLESPILALPLYRSTRRLSEEEFG
GFRIGNGEVRGRKAAAM

Signal Peptide:

amino acids 1-18

N-glycosylation Sites:

amino acids 86-89, 132-135, 181-184

FIGURE 152

GGTCCTTAAATGGAGCAGCCGCCCTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCCTG
 CTGTCCGGCTGGTCCCGGGCTGGGCGAGCCGACCCCTACTCTCTTTGCTATGACATCACCCT
 CATCCCTAAGTTTACAGACCTGGACACGCGTGGTGTGCGGTTCAAGGCCAGTGGATGAAAAGA
 CTTTTCTTCACTATGACTGTGGCAACAAGACAGTCACACCTGTCACTCCCTGGGGAAGAAA
 CTAATATGCACAACGGCCTGGAAAGCACAGAACCAGTACTGAGAGAGGTGGTGGACATACT
 TACAGAGCAACTGCGTGACATTCAGCTGGAGAATTACACACCAAGGAACCCCTCACCTGC
 AGGCAAGGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTCAGT
 TTCGATGGGCAGATCTTCTCCTCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCC
 TGGAGCCAGAAAGATGAAAGAAAAGTGGGAGAATGACAAGGTGTGGCCATGTCCTTCCATT
 ACTTCTCAATGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGGCATGGACAGCACC
 CTGGAGCCAAGTGCAGGAGCACCCTCGCCATGTCCTCAGGCAACCCCACTCAGGGCCAC
 AGCCACCACCCCTCATCCTTTGTGCTCCTCATCATCCTCCCTGCTTCATCCTCCCTGGCA
 TCTGAGGAGAGTCCCTTAGAGTGACAGGTTAAAGCTGATACAAAAAGGCTCCTGTGAGCACG
 GTCTTGATCAAACCTCGCCCTTCTGTCTGGCCAGTGCCACGACCTACGGTGTATGTCCAGT
 GGCCTCCAGCAGATCATGATGACATCATGGACCAATAGCTCATTCACTGCCTTGATTCCCTT
 TTGCCAACAAATTTTACCAGCAGTTATACCTAACATATTATGCAATTTTCTCTTGGTGTACC
 TGATGGAATTCCTGCACCTAAAGTTCTGGCTGACTAAACAAGATATATCATTTTCTTTCTTC
 TCTTTTGTGTTGGAAAATCAAGTACTTCTTTGAATGATGATCTCTTTCTTGGCAAATGATATT
 GTCAGTAAAATAATCACGTTAGACTTCAGACCTCTGGGGATTCTTTCCGTGTCCTGAAAGAG
 AATTTTTAAATTATTTAATAAGAAAAAATTTATATTAATGATTGTTTCCTTTAGTAATTTAT
 TGTCTGTACTGATATTTAAATAAAGAGTTCTATTTCCCAAAAAAAAAAAAAAAAAAAAA

FIGURE 153

MAAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVIPKFRPGPRWCQVQGQVDEKTF
HYDCGNKTVTPVSPGLGKKLVTTAWKAQNPVLREVVDILTEQLRDIQLENYTPKEPLTLQAR
MSCEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAMSFHYFS
MGDCIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLILCCLLIILPCFILPGI

Important features:**Signal peptide:**

amino acids 1-25

Transmembrane domain:

amino acids 224-246

N-glycosylation site.

amino acids 68-72, 82-86

N-myristoylation site.

amino acids 200-206, 210-216

Amidation site.

amino acids 77-81

FIGURE 154

GGGAAAGCCATTTGAAAAACCCATCTATACAACTATATATTTTCATTTCTGCTGCTAGCTG
 CCTTGGGCCTCACAAATTTTCATTCTGTTTTCTGACTTTCAAGTTATATACCGTGGAA**ATGG**GAG
 TTGATCCCAACCATAACATCGTGGAGGGTTTAAATTTTGGTGGTAGCCCTCACCCAATTCTG
 GTGTGGCTTTCTTTGCAGAGGATTCCACCTTCAAAATCATGAACTCTGGCTGTTGATCAAAA
 GAGAATTTGGATTCTACTCTAAAAGTCAATATAGGACTTGGCAAAAGAAGCTAGCAGAAGAC
 TCAACCTGGCCTCCCATAAACAGGACAGATTATTCAGGTGATGGCAAAAATGGATTCTACAT
 CAACGGAGGCTATGAAAGCCATGAACAGATTCCAAAAAGAAAAC**TCAA**ATTGGGAGGCCAAC
 CCACAGAACAGCATTTCTGGGCCAGGCTG**TAA**TCAGAATTGTCGTCGTACATGCTCAACAGC
 ATTGCTTTTTTCCCCAAAATTAACACATTGTGGAGAAGTGATGATACTCTCCCCTTACCTTT
 CCTCTCTCCATTCAAGCATTCAAAGTATATTTTCAATGAATTAACCTTGCAGCAAGGGACC
 TTAGATAGGCTTATTCTGACTGTATGCTTTACCAATGAGAGAAAAAAATGCATTTCCTGTAT
 CATCCTTTTCAATAAACTGTATTTCATTTTGAAAAAAAAAAAAAAAAAAAAA

FIGURE 155

MELIPTITSWRVLILVVALTQFWCGFLCRGFHLQNHFWLLIKREFGFYSKSQYRTWQKKLA
EDSTWPPINRTDYSGDGKNGFYINGGYESHEQIPKRRLKLGQPTQHFWARL

FIGURE 156

GTTCTCCTTTCCGAGCCAAAATCCCAGGCGATGGTGAATTATGAACGTGCCACACCATGAAG
 CTCTTTGTTGGCAGGTAACGTGTGCACCACCACACCTGGAAATGCCATCCTGCTCCCGTTCTGCTA
 CCTCACGGCGCAAGTGTGGATTCTGTGTGCAGCCATCGCTGCTGCCGCCTCAGCCGGGCCCC
 AGAACTGCCCTCCGTTTGGCTCGTGCAGTAACCAAGTTCAAGCAAGGTGGTGTGCACGCGCCGG
 GGCTCTCCGAGGTCCCGCAGGTATTCCCTCGAACACCCGGTACCTCAACCTCATGGAGAA
 CAACATCCAGATGATCCAGGCCGACACCTTCCGCCACCTCCACCACCTGGAGGTCTCTGCAGT
 TGGGCAGGAATCCATCCGGCAGATTGAGGTGGGGCCCTTCAACGGCTGGCCAGCCCTCAAC
 ACCCTGGAGCTGTTTCGACAACTGGCTGACAGTCATCCCTAGCGGGGCCCTTGAATACCTGTC
 CAAGCTCGGGAGCTCTGGCTTCGCAACAACCCCATCGAAAGCATCCCCCTTTACGCGTTCA
 ACCGGGTGCCCTCCCTCATGCGCTGGACTTGGGGGAGCTCAAGAAGCTGGAGTATATCTCT
 GAGGGAGCTTTTGAGGGGCTGTCAACCTCAAGTATCTGAACCTGGGCATGTGCAACATTAA
 AGACATGCCCAATCTCACCCCTTGGTGGGGCTGGAGGAGCTGGAGATGTGAGGGAACCACT
 TCCTTGAGATCAGGCTGGCTCCTTCCATGGCTGAGCTCCCTCAAGAAGCTCTGGGTCATG
 AACTCACAGGTCAGCCTGATTGAGCGGAATGCTTTTGACGGGCTGGCTTCACTTGTGGAACT
 CAACCTTGGCCCAATAAACCCTCTCTTCTTTGCCCATGACCTCTTTACCCCGCTGAGGTACC
 TGGTGGAGTTGCATACACCACAACCCCTTGGAACTGTGATTGTGACATTCTGTGGCTAGCC
 TGGTGGCTTGCAGAGTATATACCACCAATTCACCTGCTGTGGCCGCTGTCATGCTCCCAT
 GCACATGCGAGGCCGCTACCTCGTGGAGGTGGACAGGCCCTCCTCCAGTGCTCTGCCCCCT
 TCATCATGGACGCACCTCGAGACCTCAACATTTCTGAGGGTCGGATGGCAGAACTTAAGTGT
 CGGACTCCCCCTATGTCTCCGTGAAGTGGTGTGCTGCCAATGGGACAGTGCTCAGCCACGC
 CTCCCGCCACCAAGGATCTCTGTCTCAACGACGGCACCTTGAACTTTCCCACGTGCTGC
 TTTTCAGACACTGGGGTGTACACATGCATGGTGACCAATGTTGACGGCAACTCCAACGCCCTCG
 GCCTACCTCAATGTGAGCAGCGGTGAGCTTAACACCTCCAACATACAGCTTCTTCCACACAGT
 AACAGTGGAGACCACGGAGATCTCGCTGAGGACACAACGCGAAAGTACAAGCCTGTTCCCTA
 CCACGTCCACTGGTTACGAGCGGCATATACCACTCTACCACGGTGCTCATTTAGACTACC
 CGTGTGCCAAGCAGGTGGCAGTACCCGCGACAGACCACTGACAAGATGCAGACCAGCCT
 GGATGAAGTCATGAAGACCACCAAGATCATATTGGCTGCTTTGTGGCAGTGACTCTGCTAG
 CTGCCGCCATGTTGATTGTCTTCTATAAACTTCGTAAGCGGCACAGCAGCGGAGTACAGTC
 ACAGCCGCCCGGACTGTTGAGATAATCCAGGTGGACGAAGACATCCGAGCAGCAACATCCCG
 AGCAGCAACAGCAGCTCCGTCCGGTGATCAGGTGAGGGGCGAGTAGTGCTGCCACAATTC
 ATGACCATATTAACTACAACACCTACAACACAGCATAAGGGGCCACTGGACAGAAAACAGC
 CTGGGGAACCTCTCTGACCCCAAGTCAACCATATCTGTAACCTTATATAATTCAGACCCA
 TACCAAGGACAAGGTACAGGAACTCAAATATGACTCCCTCCCCCAAAAACCTTATAAAAT
 GCAATAGAATGCACACAAAGACAGCAACTTTTGTACAGAGTGGGGAGAGACTTTTTCTTGTA
 TATGCTTATATATTAAAGTCTATGGGCTGGTTAAAAAAAACAGATTATATTAATAATTTAAAGA
 CAAAAAGTCAAAACA

FIGURE 157

MKLLWQVTVHHHTWNAILLPFVYLTAQVWILCAAIAAAASAGPQNCPSVCSCSNQFSKVVCT
RRGLSEVPQGIPSNTRYLNLMMENNIQMIQADTFRHLHHLEVLQLGRNSIRQIEVGAFNGLAS
LNTLELFDNWLTVIPSGAFEYLSKLRELWLRNNPIESIPSYAFNRVPSLMRLDLGELKKLEY
ISEGAFEGFLFNLYNLGMCNIKDMPNLTPLVGLEELEMNGHFPFIRPGSFHGLSSLKKLW
VMNSQVSLIERNAFDGLASLVELNLAHNNLSSLPHDLFTPLRYLVELHLHHNPWNCDLILW
LAWWLREYIPTNSTCCGRCHAPMHRGRYLVEVDQASFCQCSAPFIMDAPRDLNISEGRMAEL
KCRTPPMSSVKWLLPNGTVLSHASRHRPRISVLNDGTLNFSHVLLSDTGVTTCMVTNVAGNSN
ASAYLNVSTAEINTSNYSFFTIVTVETTEISPEDTTRKYKVPVPTTSTGYQPAYTTSTTVLIQ
TTRVPKQVAVPATDTTDMQTSLEVMKTTKIIIGCFVAVTLAAAMLIVFYKLRKRHQORS
TVTAARTVEIIQVDEDIPAATSAAATAAPSGVSGEGAVVLP TIHDHINYNTYKPAHGAHWTE
NSLGNLSLHPTVTTISEPYIIQTHTKDKVQETQI

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FIGURE 158

CGCTCGGGCACCAGCCGCGGCAAGG**ATG**GAGCTGGGTGCTGGACGAGTTGGGGCTCACTTTTCTTCAGCTCC
 TTCTCATCTCGTCTTCCGAAGAGATACACAGTCATTATGAAGCCTGCCCTGGAGCAGAGTGGAAATATCATG
 TGTGCGGAGTGTGTGAATATGATCAGATTGAGTGCCTCTGCCCCGGAAGAGGGAAGTCTGTGGTTATACCAT
 CCTTGTCTGAGGAATGAGGAGATGAGTGTGACTCCTGCCTGATCCACCCAGGTTGTACCTCTTTGAAAAT
 GCAAGAGCTGCCAAATGGCTCATGGGGGGTACCTTGGATGACTTCTATGTGAGAGGGGTCTACTGTGCAGAG
 TGCCGAGCAGGGCTGTACGGAGGAGACTGCATGCGATGTGGCCAGGTTCTGCGAGCCCCAAGGGTCAGATTTT
 GTTGGAAAGCTATCCCTAAATGCTCACTGTGAATGGACCATTCATGCTAAACCTGGGTTTGTCACTCCAACTAA
 GATTTGTCTATCTTGAGTCTGGAGTTTGACTACATCTGCCAGTATGACTATGTTGAGGTTCTGTGATGGAGCAAC
 CCGGATGCCAGATCATCAAGCGTCTCTGTGGCAACGAGCGGCCAGCTCCTATCCAGAGCATAGGATCCTCACT
 CCACTCTCTTCCACTCCGATGGCTCCAAGAATTTGACGGTTTCCATGCCATTTATGAGGAGATCAGAGCAT
 GCTCCTCATCCCCTTGTTTCCATGACGGCAGCTGCGTCTTGACAAAGGCTGGATCTTACAAGTGTGCCTGCTTG
 GCAGGCTATACTGGGCAGCGCTGTGAAAATCTCCTTGAGAAAGAACTGCTCAGACCCCTGGGGGCCAGTCAA
 TGGGTACCGAAAAATAACAGGGGGCCCTGGGCTTATCAACGGACGCCATGCTAAAATTGGCACCCCTGGTGTCTT
 TCTTTTGTAACTCCTATGTTCTTAGTGGCAATGAGAAAAGAACTTGCCAGCAGAATGGAGAGTGGTCAGGG
 AAACAGCCCATCTGCATAAAGCCTGCCGAGAACCAAGATTTCAGACCTGGTGAGAGGAGAGATTCTCCGAT
 GCAGGTTTCACTCAAGGAGACACCAATTACACAGCTATACTCAGCGGCTTCAGCAAGCAGAACTGCAGAGTG
 CCCCACCAAGAGGCCAGCCCTTCCCTTTGGAGATCTGCCATGGGATACCAACATCTGCATACCCAGCTCCAG
 TATGAGTGCATCTCACCTTCTACCGCCGCTGGGCAGCAGCAGGAGGACATGTCTGAGGACTGGGAAGTGGAG
 TGGCGGGCACCATTCTGCATCCCTATCTGCGGGAAAATTGAGAACATCACTGCTCCAAAGACCCAGGGTTGC
 GCTGCGCGTGGCAGGCAGCCATCTACAGGAGGACAGCGGGGTGCATGACGGCAGCTACACAAGGAGCGTGG
 TTCTAGTCTGCAGCGGTGCCCTGGTGAATGAGCGCACTGTGGTGGTGGCTGCCACTGTGTTACTGACCTGGG
 GAAAGTACCATGATCAAGACAGCAGACCTGAAAGTTGTTTGGGGAAATTCTACCGGGATGATGACCGGGATG
 AGAAGACCATCCAGAGCCTACAGATTCTGCTATCATCTGCATCCCAACTATGACCCCATCTGCTTGTATGCT
 GACATCGCCATCCTGAAGCTCTAGACAAGGCCGCTATCAGCACCCGAGTCCAGCCCATCTGCCTGCTGCCAG
 TCGGGATCTCAGCACTTCTTCCAGGAGTCCACATCACTGTGGCTGGCTGGAAATGCTCTGGCAGAGCTGAGGA
 GCCCTGGCTTCAAGAACGACACACTGCGCTCTGGGGTGGTCACTGTGGTGGATCGCTGCTGTGTGAGGAGCAG
 CATGAGGACCATGGCATCCAGTGAGTGTCACTGATAACATGTTCTGTGCCAGCTGGGAACCCACTGCCCTTC
 TGATATCTGCACTGCAGAGACAGGAGGCATCGCGGCTGTGCTCTCCCGGAGCAGCATCTCTGAGCCAGGCT
 GGCATCTGATGGGACTGTGCTAGCTGGAGCTATGATAAAACATGCGGCCACAGGCTCTCCATGCCCTTCCACAG
 GTGCTGCCCTTTTAAAGACTGGATTGAAAGAAATATGAAAT**TGA**ACCATGCTCATGCACTCCTTGAGAAGTGTTC
 TGTATATCCGCTCTGTACGTGTGCATTGCGTGAAGCAGTGTGGGCTGAAGTGTGATTGGCCTGTGAACCTTGG
 CTGTGCCAGGGCTCTTGACTTCAGGGACAAACATCACTGAGGGGTGAGTAGACCTCCATTGCTGTGATGCTCAT
 CGCCGCTCCACTACTAGGACAGCCAAATGGAAGTGGCAGGGCTTGCAGAGTAAGTTCCTTCAAGAGAGAC
 ATATACAAACCTCTCCACTCCAGCTGACCTGGTGGCTTCCCAACTTCAGTTATACGAATGCCATGCTGTTG
 ACCAGGGAAGATCTGGGCTTCATGAGGCCCTTTTGAGGCTCTCAAGTTGAGAGCTGCCGTGGGACAGCC
 GCGGCACAGAGCTGGATGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
 CCATCTCTTGTACACATTTTAAATAAAATAGGGTTGGCTCTGAACATACAAAAAATAAAAAAATAAAAAA
 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA
 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA

FIGURE 159

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECCEYDQIECVCPGKREV
GYTIPCCRNEENECDSLHPGCTIFENCKSCRNGSWGGLDDFYVKGIFYCAECRAGWYGGD
CMRCGQVLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRD
GDNRDGQIIKRVCGNERPAPIQSIGSSLHVLPHSDGSKNFDGFHAIYEEITACSSSPCFHDG
TCVLDKAGSYKCACLAGYTQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTV
VSFFCNSYVLSGNEKRTCQONGEWGSKQPICIKACREPKISDLVRRRLVPMQVQSRETPLH
QLYSAAFSKQKLQSAPTCKKPALPFGDLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGK
WSGRAPSCIPICGIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNE
RTVVVAACHCVTDLGKVTMIKTADLKVVLGKFYRDDDRDEKTIQSLQISAILHPNYDPILLD
ADIAILKLLDKARISTRVQPICLAASRDLSFSQESHITVAGWNVLADVRSPGFKNDTLRSG
VVSVDLSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDICTAETGGIAAVSFPGRASPEPR
WHLMGLVSWSYDKTCSHRLSTAFTKVLFPKDWIERNMK

FIGURE 160

ACCAGGCATTGTATCTTCAGTTGTCATCAAGTTCGCAATCAGATTGGAAAAGCTCAACTTGA
 AGCTTTCTTGCTGCAGTGAAGCAGAGAGATAGATATTATTCACGTAATAAAAAACATGGGC
 TTCAACCTGACTTTCCACCTTTCCCTACAAATTCGATTACTGTTGCTGTTGACTTTGTGCCT
 GACAGTGGTTGGTGGCCACCAGTAACCTACTTCGTGGGTGCCATTCAAGAGATTCCCTAAAG
 CAAAGGAGTTCATGGCTAATTTCCATAAGACCCCTCATTTTGGGGAAGGGAAAACTCTGACT
 AATGAAGCATCCACGAAGAAGGTAGAAGTTGACAACTGTCCTTCTGTGCTCCTTACCTCAG
 AGGCCAGAGCAAGCTCATTTTCAAACCAGATCTCACTTTGGAAGAGGTACAGGCAGAAAATC
 CCAAAGTGTCCAGAGGCCGGTATCGCCCTCAGGAATGTAAAGCTTTACAGAGGGTCGCCATC
 CTCGTTCCCCACCGAACAGAGAGAAACCTGATGTACCTGCTGGAACATCTGCATCCCTT
 CCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCATCCACCAGGCTGAAGGTAAAAAGT
 TTAATCGAGCCAAACTCTTGAATGTGGCTATCTAGAAGCCCTCAAGGAAGAAAATTGGGAC
 TGCTTTATATPCCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGA
 GGAGCATCCCAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTG
 GATATTTTGGGGGTGTTACTGCCCTAAGCAGAGAGCAGTTTTTCAAGGTGAATGGATTCTCT
 AACAACTACTGGGGATGGGGAGGCCAAGACGATGACCTCAGACTCAGGGTTGAGCTCCAAAG
 AATGAAAATTTCCGGCCCTGCCTGAAGTGGTAAATATACAATGGTCTTCCACACATAGAG
 ACAAAGGCAATGAGGTGAACGCAGAACGGATGAAGCTCTTACACCAAGTGTACAGAGTCTGG
 AGAACAGATGGGTTGAGTAGTTGTTCTTATAAATTAGTATCTGTGGAACACAATCCTTTATA
 TATCAACATCAGAGTGGATTTCTGGTTTGGTGCATGACCCTGGATCTTTTGGTGATGTTGG
 AAGAACTGATCTTTGTTTGCATAATTTTGGCCTAGAGACTTCAAATAGTAGCACACATTA
 AGAACCTGTTACAGCTCATTGTTGAGCTGAATTTTTCCTTTTGTATTTTCTTAGCAGAGCT
 CCTGGTGATGTAGAGTATAAACAGTTGTAACAAGACAGCTTCTTAGTCATTTTGATCATG
 AGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAAGGATGACTCAAAGGAT
 AAAATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTTATTTAAATTTGAAGTAATATAT
 TATGGGATAAAAGGCCACAGGAATAAGACTGCTGAATGTCTGAGAGAACCAGAGTTGTTCT
 CGTCCAAGGTAGAAAGGTACGAAGATACAATACTGTTATTCTATTTATCCTGTACAATCATCT
 GTGAAGTGGTGGTGTGAGTGAGAAGGCGTCCACAAAAGAGGGGAGAAAAGGCGACGAATCA
 GGACACAGTGAACCTGGGAATGAAGAGGTAGCAGAGGGTGGAGTGTGCGCTGCAAAGGCAG
 CAGTAGCTGAGCTGGTTGACAGGTGCTGATAGCCTTCAGGGGAGGACCTGCCCAGGTATGCCT
 TCCAGTGATGCCACCAGAGAATACATTCTCTATTAGTTTTTAAAGAGTTTTGTAAAAATGA
 TTTTGTACAAGTAGGATATGAATTAGCAGTTTACAAGTTTACATATTAACATAATAATAA
 TGTCTATCAAAATACCTCTGTAGTAAAAATGTGAAAAAGCAAA

FIGURE 161

MGFNLTfHLSYKFRLLLLLTCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLLILGKGKT
LTNEASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYRPQECKALQRV
AILVPHRNRKHLMYLLEHLHPFLQRQQLDYGIYVIHQAEKKFNRAKLLNVGYLEALKEEN
WDCFI FHDVDLVPENDFNLYKCEEHPKHLVVGRNSTGYRLRYSGYFGGVTALSREQFFKVNG
FSNNYWGWGGEDDDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVSR
VWRTDGLSSCSYKLVSV EHNPLYINITVDFWFGA

Important features:**Signal peptide:**

amino acids 1-27

N-glycosylation sites:

amino acids 4-7, 220-223 and 335-338

Xylose isomerase proteins:

amino acids 191-201

FIGURE 162

CTGGGGCCGGGGTCTGGCCAGCGGGCTGTGGGGCGCCCCGGAGGAGCGACCGCCGAGTTCTC
GAGCTCCAGCTGCATTCCTCCGCTCCGCGCCAGCCTTCTCCGCTCCGGGCCCGCCAGT**AG**
GCCAGGAGGCTGTGGTGCGCCCTCGCCGCATCTCTGGCTTGCCTGCTCTCTGCCCTGGCG
CCCCGACGGGTGGCCCGAGGCCCTGTATGAACCTAATCTACACCAGGTAGCCCTGCCACCA
CGGGAGCGGTGGTGACCATCTCGGCCAGCCTGGTGGCCAAAGGACAACGGCAGCCTGGCCCTC
CCCGTCAGCCCCACTTCTACCGCTTCCACTGGATCCACACCCCGCTGGTGCTTACTGGCAA
GATGGAGAAGGCTTCTCAGCTCCACATCGTGTGGTGGCCACGCTGCCCGGGGAATTCGCGG
TCTCTGTCTGGGTCTACGCGCTGACTGCTGGATGTGGCAGCCTGTGGCCAGGGGCTTGTG
GTCTCTCCCATCAGAGATTCTCTGTGGGGGACCTTGTGTGACCCAGAACACTTCCCTACC
TGTCGGCCAGCTCTATCTCACTAAGCCGCTGTGAAGTCTCTCTCTCTCCCTACGACCCGA
GCAACTTCTCAAGACCGCTTGTTTCTCTACAGCTGGGACTTCCGGGACGGGACCCAGATG
GTGACTGAAGACTCCGTGGTCTATTATAACTATTCCGATCTCGGGACCTTACAGGTGAAGCT
CAAACTGGTGGCGGAGTGGGAAGAGCTGGAGCCGATGCCACGAGGGCTGTGAACGAGAAGA
CCGGGGACTTCTCCGCTCGTGAAGCTCAGGAAACCTTCGAGGCATCCAAGTGTGGGG
CCCCACTTAATCAGACCTTCCAAGAAGATCACCGTGACCTTGAATCTCTGGGGAGCCCTTCT
TCTGACTGTGTCTGGGCTCTCAAGCTGAGTGCTCCCTCCGCTGGAGGAAGGGAGTGGCCACC
CTGTTCCGTGGCCAGCACAGCGTACAACCTGACCCACACCTTCAGTGACCTTGGGAGACCTAC
TGCTTCAGCATCCGGGCCGAGAAATATCATCAGCAAGACATCAGTACCACAGATTCAGGT
GTGGCCCTCCAGAAATCAGCGCGGTGCTTTGCTTTCCATGTGTCTACATTCATCACTGTGA
TGTTGGCCTTCATCATGTACATGACCCCTCGGGAATGCCATCAGCAAAAGACATGGTGAG
AACCCGAGGCCACCTCTGGGTGAGGTGCTGCTGCCAGATGTGCTGTGGGCTTTCTTGG
GGAGACTCCATCTGAGTACCTGGAATTTGTTCTGTGAGAACCCGGGCTGCTCCGCCCCCTCT
ATAAGTCTGTCAAACCTACACCGCT**TCG**CAGACCTCCCTCCCCACCCCTCTCAGTGTAA
CTGACTGCTGACTTGGAGTTTCCAGAGGGTGGTGTGCACCATGACCAGAGGGGTCACT
TGCTGGGGCTGTTGGCCTGATCATTCATCTGTACAGTTACGCACTGCCACAAGCC
CTCCCTCTCTGTACCCCTGACCCCGAGCCATCACCATCTGTACAGTCCAGCCACTGACA
TAAGCCCCACTCGGTACACCCCCCTTGACCCCTACCTTTGAAGAGGCTTCTGTGAGGACT
TTGATGCTTGGGGTGTTCCCTGTGTAACCTCTAGTGGGCTGGCTGCCCATGCCCATCTCCCT
CTCATATTGGCACATCTGCTGTCCATTGGGGTTCTCAGTTTCTCCCTCCAGACAGCCCTAC
CTGTGCCAGAGAGCTAGAAGAAGGTCTAAAGGGTTAAAAATCCATAACTAAAGTTGTAC
ACATAGATGGGCACATCAGACAGAGAAGTGTGATGTACACACACACACACACACACACA
CACACACACAGAAATATAAACATCGCTCATAGCTAGGCAATTCAGATGATCAGCTGTGA
TCTGGTTAAGTCGGTTGCTGGGATGACCCCTGCATAGAGCTGAAGAGAATTTGACCTCCA
AGAGCCCTGACAGGCTTCTGGGCCGGCGCCCTCCCTTTGTGCTTTGPTCTGCAGTTCTTGG
GCCCTTTATAAGGCCATCTAGTCCCTGCTGGCTGGCAGGGGGCTGGATGGGGGGCAGGACT
AAACTGAGTGAATTGCAGAGTGCTTTATAAATACCTAATTTATTCGAAGACCCATCTGTG
AATCACTTTCATCAGGAAAGGCTTCGACGGGTAGAAGAGGTTGAGTCAAGCCGGCGCGGTG
TGGCTACGCTTGAATCCAGCACTTTGGAGAGCCGAGGCGGGTGGATCAGAGATCAGGA
GATCAGAGACCCCTGGCTAACACGGTGAAGACCCCGTCTCTACTAAAAAATACAAAAGTT
AGCGGGCGGTGGTGGTGGGTGCTGTAGTCCAGCTACTCGGAGGCTGAGGCAGGAGAATG
GTGCAAGCCCGGGAGCGGAGCTTGAGTGAGCCACAGATGGCGCCACTGCATCAGCCTGA
GTGACAGAGCGGAGCTGTGCTTCCA

FIGURE 163

MAQAVWSRLGRILWLACLPLPAPAGVAAGLYELNLTTDSPATTGAVVTISASLVAKDNGSLA
LPADAHLYRFHWIHTPLVLTGKMEKGLSSTIRVGVHVPGEFPVSVWVTAADCWMCQFPVARG
VVLPITEFLVGLDVVTTQNTSLPWPSSYLTKTVLKVSFLLHDPNSFLKTALFLYSWDFGDGTQ
MVTEDSVVYYNYSIIGTFTVKLVVAAEWEEVEPDATRAVKQKTGDFSASLKLQETLRGIQVL
GPTLIQTQFKMTVTLNFLGSPPLTVCSWRCLKPECLPEEGECHPVSVASTAYNLTHTRDPGD
YCFISRAENIISKTHQYKGIQWPSRIQPAVFAFPCATLITVMAFIMYMLTRNATQQKDMV
ENPEPPSGVRCCOMCCGPFLELTPESEYLEIVRENHGLLPPLYKSVKTYTV

Important features of the protein:

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 339-362

N-glycosylation sites.

amino acids 34-37, 58-61, 142-145, 197-200, 300-303 and 364-367

FIGURE 164

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCACG**ATG**GCACTGAGCTCCCAGATCT
GGGCCGCTTGCCCTCCTGCTCCTCCTCCTCGCCAGCCTGACCACTGGCTCTGTTTCCCA
CAACAGACGGGACAACTTGCAGAGCTGCAACCCAGGACAGAGCTGGAGCCAGGGCCAGCTG
GATGCCCATGTTCAGAGGCGAAGGAGCGAGACCCCACTTCCCCATCTGCATTTTCTGCT
GCGGCTGCTGTATCGATCAAAGTGTGGGATGTGCTGCAAGACG**TAG**AACCTACCTGCCCTG
CCCCCGTCCCCTCCCTTCCCTTATTTATTCCTGCTGCCCAGAACATAGGTCTTGAATAAAA
TGGCTGGTTCTTTTGTTCCTTTCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAA

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FIGURE 165

MALSSQIWAACLLLLLLSLTSGSVFPQQTGQLAELQFQDRAGARASWMPMFQRRRRRDTH
FPICIFCCGCCHRSKCGMCCKT

0090427 240660

CTGTCAAGGAAGGACCATCTGAAGGCTGCAATTTGTTCTTAGGGAGGCAGGCTGCTGGCCTGGC
CTGGATCTCTCCAACT**ATG**TTCTGTTGCTGCTCTTTGATGACCGTAGTGTCAACCTCTCTGGGC
ATCTCCCTGACTGCTCTCTTCAACCTCCTTCTGCTTTTATCATATAGTGCCAGCAATTTTTGG
AGTCTCCTTTGGTATTCGCAAACTCTACATGAAAGCTCTGTTAAAAATCTTTTGGCTGGGCTA
CCTTGAGAATTGGAGCGAGGACCAAGGAAGAACCACGAGTTTACAAGCCTACACCAAC
GGAATCATTTGCAAGGATCCCACTTCTACTAGAAGAAGATCAAGAAGATCTGCGAAGTGG
TAGTAGTAAGGCTCTGCAACAACACTCCAGATGTCCAGCTCTGACATTTTCTACTTTTCG
GGAAGAAGATGGAGACCATATGATGATGAGGTGACAAAGAAGATCTTCAAGCAAGAAGCTG
GAGTCTTGGAACCTGCTGAGCAGAACCAATTATAACTTCCAGTACATCAGCCTTCGGCTCAC
GGTCTGTGGGGGTTAGGAGTGCTGATTCGGTATCTGTTTCTGCTGGCTCAGGATAGCACT
TGGCTTTCACAGGAGTATGCTTTCTGGTGGTGGGCACACTGTGGTGGGATACTTGCCAAAT
GGGAGGTTTAAAGAAATTCATAGTAAACATGTTCACTTAATGTGTTACCGGATCTGCGTGGC
AGGCTGACAGCCATCATCTACCTACCATGACAGGGAAACACCAAGAAATGGTGCCATCT
GTGTGGCCAAATCATACCTACCGATCGATGCTGATCATCTGGCCAGCGATGCTATTATGCC
ATGTTGGGTCAAGTGCACGGGGGACTCATGGGTGTGATTCAAGAGACCGATGTTGAAGCCTG
CCCAACGCTGTGGTTGGAGCGCTCGAAGTGAAGATGCCCACTGGTGGCTTAAGAGACTGA
CTGAACATGCTGCAAGATAAAGCAAGCTGCCTTCACTTCTTCCAGAAAGAACCTGCATC
AATAATACATCGGTGATGATGTTCAAAAAGGAGGTTTGAATATGGAGCCACGTTTACCT
TGTTGCTATCAAGATGACCTCAATTTGGCGATGCCCTTGCAACAGCAGCAAAATACGGGA
GGGTGACGTCATCTGCTCGAATGATACCAAGCTGGGCCATGTTCTGACGCTGTGTGCTACCT
CTCCCATGACTAGGAGGCGAGATGAAGATGCTGTCCAGTTTGGCAATAGGTTGAATCTGCG
CATTGCCAGGCAGGGAGGACTTGTGGACCTGCTGTGGGATGGGGGCTGAAGAGGGAGAAGT
TGAAGGACACGTTCAAGGAGGAGCAGCAGAGCTGTACAGCAAGATGATCTGTGGGAACCAAC
AAGACAGGAGCGCTCT**TGA**CGCTGCCCTCCAGTGGCTGGGCGACCGCTGCGGGTGCCAA
CGGCTCGAGAGCTGGAAGTGGCCGCGCGCGGCCCACTGCTGTGCTCTTCCAGACTCCAGG
CTCCCCGGGCTGCTCTGATCCAGACTCCGGCTTCCGCGAGCCGACGGGATCCCTGT
GCACCCGGCGCAGCCTACCTTGGTGGTCTAAACGGATGCTGCTGGTGTGGCGACCCAGGA
CGAGATGCCCTGTTTCTTTTCAATTAAGTCTGTGGAGAATGCCATTAAGTGAATCCCCA
CCTTTGACAGCTGTGCGGGCTGAGTGGTTGGGAGATGTGGCCATGTGTTGTGCTAGAGAT
GGCGGTACAAGAGTCTGATTATGCAAGCCGTGTGCCAAGGGATGTGCTGGGGGCGGCCACCG
CTCTCCAGGAAGAAGCAGCTGAGGCATGTGGCTGGCTTCCGCTCAACATCTGCCCCAGC
CTTGAGCTCTGCAGACATGATAGGAAGGAACTGTCACTCGCAGGGGCTTTCAAGCAAAATG
AAGGGTTAGATTTTATGTGCTGCTGCTGAGTGGGTTACTAAAGGGAGGGGACAGGCGAGGTG
GGCGCTGACTGGGCCATGGGGAAGAACGTTGTGTTCTGCTACAGGCTAACCTGAACTCCC
ATGTGATGCGCGCTTTGTTGAATGTGTGCTCGGTTTCCCCATCTGTAATATGAGTCGGGG
GAATGGTGGTGATTTCACTACCTCACAGGGCTGTTGTGGGATTAAGGTGTCGCGGTGAGTGA
AGGACACATCAAGTTCAGTGGTTTCAAGTACAGGCCCAAAACGGGCGACGCGAGCCCTGAG
CTCAGAGTGTCTGCATGGGCTTTGGATTTGTTCTTGTGAGTAAATAAACTGGCTGGTGAA
TGA

FIGURE 167

MFLLLPFDSLIVNLLGISLTVLFTLLLVFIIIVPAIFGVSTFGIRKLYMKSLLKIFAWATLRME
RGAKEKNHQLYKPYTNGIIAKDPTSLEEEIKEIRRGSSKALDNTPEFELSIFYFCRKGME
TIMDDEVTKRFSAEELSWNLLSRNTYNFYISLRLTVLWGLGVLIKYCFLLPLRIALFTG
ISLLVVGTTVGYLPNGRFKEFMSKHVHLMCYRICVRALTAITYHDRENRPNGGICVANH
TSPIDVILASDGYAMVGQVHGGLMGVIQRAMVKACPHVWFERSEVKDRHLVAKRLTEHVQ
DKSKLPILIFPEGTCINNTSVMFKKGSFEIGATVYPVAIKYDPQFGDAFWNSSKYGMVTYL
LRMMTSWAIVCSVWYLPMPMTREADEDAVQFANRVKSAIARQGGLVDLLWDGGLKREKVKDTF
KEEQQKLYSKMIVGNHKDRSRS

FIGURE 168

GCCCCTCGAAACCAGGACTCCAGCACCTCTGGTCCCGCCCTCACCCGACCCCTGGCCCTCA
 CGTCTCCTCCAGGGATGCGCTGGCGGCTTTGATGATCGCCCTCGGCAGCCTCGGCCCTCCAC
 ACCTGGCAGGCCCAGGCTGTTCCACCATCCTGCCCCTGGGCCTGGCTCCAGACACCTTTGA
 CGATACCTATGTGGGTTGTGCAGAGGAGATGGAGGAGAAGGCAGCCCCCTGCTAAAGGAGG
 AAATGGCCCACCATGCCCTGCTGCGGGAATCCTGGGAGGCAGCCCAGGAGACCTGGGAGGAC
 AAGCGTCGAGGGCTTACCTTGCCCCCTGGCTTCAAAGCCCAGAATGGAATAGCCATTATGGT
 CTACACCAACTCATCGAACACCTTGTA CTGGGAGTTGAATCAGGCCGTGCGGACGGGCGGAG
 GCTCCCGGAGCTCTACATGAGGCACTTTCCCTTCAAGGCCCTGCATTTCTACCTGATCCGG
 GCCCTGCAGCTGCTGCGAGGCAGTGGGGGCTGCAGCAGGGGACCTGGGAGGTGGTGTCCG
 AGGTGTGGGCAGCCTTCGCTTTGAACCCAAAGAGGCTGGGGGACTCTGTCCGCTTGGGCCAGT
 TTGCCTCCAGCTCCCTGGATAAGGCAGTGGCCACAGATTTGGGGAGAAGAGCGGGGCTGT
 GTGTCTGCGCCAGGGGTGCAGCTAGGGTCACAATCTGAGGGGGCCTCCTCTCTGCCCCCCTG
 GAAGACTCTGCTCTTGCCCCCTGGAGAGTTCCAGCTCTCAGGGGTGGGGCCTGAAAGTCCA
 ACATCTGCCACTTAGGAGCCCTGGGAACGGGTGACCTTCATATGACGAAGAGGCACCTCCAG
 CAGCCTTGAGAAGCAAGAACATGGTTCCGGACCCAGCCCTAGCAGCCTTCTCCCAACCAGG
 ATGTTGGCCTGGGGAGGCCACAGCAGGGCTGAGGGAATCTGCTATGTGATGGGGACTTCCT
 GGGACAAGCAAGGAAAGTACTGAGGCAGCCACTTGATTGAACGGTGTGCAATGTGGAGACA
 TGGAGTTTATTGAGGTAGCTACGTGATTAAATGGTATTGCAGTGTGGA

FIGURE 169

MALAALMIALGSLGLHTWQAQAVPTILPLGLAPDTFDDTYVGCAEEMEEKAAPLLKEEMAHH
ALLRESWEAAQETWEDKRRGLTLPFGFKAQNGIAIMVYTNSNTLYWELNQAVRTGGGSREL
YMRHFPPKALHFYLIRALQLLRSGGCSRGPGEVVFVRGVGSLRFEPKRLGDSVRLGQFASSS
LDKAVAHRFGEKRRGCVSAPGVQLGSQSEGASSLPWKTILLAPGEFQLSGVGP

FIGURE 170

GTGGCTTCATTTAGTGGCTGACTTCCAGAGAGCAAT**ATG**GCTGGTTCCCCAACATGCCTCA
CCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTG
GTCGGTTCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTC
TATTGTCTGGACCTTCAACACAACCCCTCTTGTACCATAACAGCCAGAAGGGGGCACTATCA
TAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCAGATGGAGGCTACTCCCTGAAG
CTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACT
CCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAG
TCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATG
GAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTC
CCATAATGGGTCCATCCTCCCCATCTCCTGGAGATGGGGAGAAAGTGATATGACCTTCATCT
GCGTTGCCAGGAACCTGTGAGCAGAACTTCTCAAGCCCCATCCTTGCCAGGAAGCTCTGT
GAAGGTGCTGCTGATGACCCAGATTCTCCATGGTCCTCCTGTGTCTCCTGTTGGTGCCCTT
CCTGCTCAGTCTCTTGTACTGGGGCTATTTCTTTGGTTTCTGAAGAGAGAGAGACAAGAAG
AGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTGCGGAAACTCCTAACATATGCCCCCAT
TCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAATAGAACAACTCCTAAAGGAAGA
TCCAGCAAATACGGTTTACTCCACTGTGGAATATACCGAAAAAGATGGAAAAATCCCCACTCAC
TGCTCACGATGCCAGACACACCAAGGCTATTTGCCTATGAGAATGTTAT**CTAG**ACAGCAGTG
CACTCCCCTAAGTCTCTGCTCA

FIGURE 171

MAGSPTCLTLIYLWQLTGSAAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVT
IQPEGGTIIIVTQNNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHV
YEHLSPKPVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSILPISWRW
GESDMTFICVARNPVS RNFS SPILARKLCEGAADDPDSSMVLCLLLVPLLLSLFVLGLFLW
FLKRERQEEYIEEKKRVDICRETPNICPHSGENT EYDTIPHTNRILTILKEDPANTVYSTVEIP
KKMENPHSLLTMPDTPRLFAYENVI

CTGTGTTCCCCAACATGCGCTCACCCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCC
TCTGGACCCGTGAAAGAGCTGGTCCGTTCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTC
CAAAGTAAAGCAAGTTGACTCTATTGTCTGGACCTTCAACACAACCCCTCTGTGCACCATAC
AGCCAGAAGGGGGC~~ACT~~ATCATAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCA
GATGGAGGCTACTCCCTGAAGCTCAGCAA~~ACT~~GAAGAAGATGACTCAGGGATCTACTATGT
GGGGATATACAGCTCATCACTCCAGCAGCCCTCACCAGGAGTACGTGCTGCATGCTTACG
AGCACCCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTG
ACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCT
GGGGCAAGCAGCCAATGAGTCCCATAAATGGGTCCATCCTCCCATCTCCTGGAGATGGGGAG
AAAGTGATATGACCTTCACTCGCTTGCCAGGAACCCTGTCAGCAGAA~~ACT~~TCTCAAGCCCC
ATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCATGGTCTCCTCT
GTGTCCTCTGTTGGTGCCCCCTCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTC
TGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTCTGGGAA
ACTCCTAACATATGCCCCCATCTCTGGAGAGAAACAGAGTACGACACA~~ACT~~CCCTCACACTAA
TAGAACAACCTCTAAAGGAAGATCCGACAAATACGGTTTACTCCACTGTGGAATACCGAAAA
AGATGGA~~AAAT~~CCCCCATCTACTGCTCAGTAGCGAGACACCAAGGCTAATTTGCCATATGAG
AATGTTATCTAGACAGCAGTGCACCTCCCTTAAGTCTCTGCTCAAAAAAAAAAAAAAAAAAAAA

FIGURE 173

GAAAGACGTGGTCCTGACAGACAGACAATCCTATTCCCTACCAAA**ATG**AAGATGCTGCTGCT
GCTGTGTTTGGGACTGACCCTAGTCTGTGTCCATGCAGAAGAAGCTAGTTCTACGGGAAGGA
ACTTTAATGTAGAAAAGATTAATGGGGAATGGCATACTATTATCCTGGCCTCTGACAAAAGA
GAAAAGATAGAAGAACATGGCAACTTTAGACTTTTTCTGGAGCAAATCCATGTCTTGGAGAA
TTCCTTAGTTCTTAAAGTCCATACTGTAAGAGATGAAGAGTGTCCGAATTATCTATGGTTG
CTGACAAAACAGAAAAGGCTGGTGAATATTCTGTGACGTATGATGGATTCAATACATTACT
ATACCTAAGACAGACTATGATAACTTTCTTATGGCTCACCTCATTAAACGAAAAGGATGGGGA
AACCTTCCAGCTGATGGGGCTCTATGGCCGAGAACCAGATTTGAGTTCAGACATCAAGGAAA
GGTTTGCACAACTATGTGAGGAGCATGGAATCCTTAGAGAAAATATCATTGACCTATCCAAT
GCCAATCGCTGCCTCCAGGCCCAGAAATGAAGAATGGCCTGAGCCTCCAGTGTTGAGTGGAC
ACTTCTCACCAGGACTCCACCATCATCCCTTCCTATCCATACAGCATCCCCAGTATAAATTC
TGTGATCTGCATTCCATCCTGTCTCACTGAGAAGTCCAATTCCAGTCTATCAACATGTTACC
TAGGATACCTCATCAAGAATCAAAGACTTCTTTAAATTTCTCTTTGATACCCCTTGACAAAT
TTTTCATGAAATTATTCCTCTTCCTGTTCAATAAATGATTACCCTTGCACTTAA

FIGURE 174

MKMLLLLCGLTLVCVHAEASSTGRNFNVEKINGEWHTIILASDKREKIEEHGNFRLFLEQ
IHVLENSLVLVKHTVRDEECSELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDNFLMAHLI
NEKDGETFQLMGLYGREPDLSDDIKERFAQLCEEHGILRENIIDLSNANRCLQARE

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GGGCTCGAGCGTTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAA
TGGATTACAGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTG
TCAGCTTAGTTGAGGAAGACCAATTTTCTCAAACCCCATCTCTTGCTTTGAGTGGTGGTTT
CCAGGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCAAG
AAAAAGAGCGTGCTGCAACAACAGAACTGGAATGTTTCTTTTCATCATTTTTTCAGTGTGATCA
CAGTCATTGGTGTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAGGTCCTCTC
ATGTGTAATTCTCCAAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGA
CATTTCATCCAGAATCCTTCAACTTGCAGTGGTTTTTCAATGACTCTTGTGCACCTCCTACTG
GTTTCAATAAACCACCAGTAACGACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCAC
TTCGATTCTGAAGAAAAACAACATAGGCTTATCCACTTCTCAGTATTTTTAGGTCATTGCT
TGTGGGAATCTCTGGAGGTCCTGTTTGGGCTCAGTCAGATAGTCATCGGTTTCCCTGGCTGTC
TGCTGGAGTCTCTTAAGCGAAGAGTCAAATTGTGTAGTTTAATGGGAATAAAATGTAAGTA
TCAGTAGTTTGAAAAAAAA

MTCCEGWTSCTNGFSLVLLVLLLVVLLNAIPLIVLSVEEDQFSQNPISCFEWWFPGIIGAGLMA
 IPATMTSLTARKACNNRTGMFLSSFFSVITVIGALYCLISIQALLKGPLMCSNPSNSNA
 NCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGRWRASSFHFDFSEENKHLR
 IHFSVFLGLLLVGILEVLVFLGLSQIVIGFLGCLCGVSKRRSQIV

FIGURE 177

GTCGAATCCAAATCACTCATTGTGAAAGCTGAGCTCACAGCCGAATAAGCCACCATGAGGCT
GTCAGTGTGTCTCCTGATGGTCTCGCTGGCCCTTTGCTGCTACCAGGCCCATGCTCTTGCTCT
GCCCAGCTGTTGCTTCTGAGATCACAGTCTTCTTATTCTTAAGTGACGCTGCGGTAAACCTC
CAAGTTGCCAAACTTAATCCACCTCCAGAAGCTCTTGACGCCAAGTTGGAAGTGAAGCACTG
CACCGATCAGATATCTTTTAAAGAAACGACTCTCATTGAAAAAGTCCTGGTGGAAATAGTGAA
AAAAATGTGGTGTGTGACATGTAAAAATGCTCAACCTGGTTTCCAAAGTCTTTCAACGACACC
CTGATCTTCACTAAAAATTGTAAAGGTTTCAACACGTTGCTTTAATAAATCACTTGCCCTGC

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FIGURE 178

MRLSVCLLMVSLALCCYQAHALVCPAVASEITVFLFLSDAAVNLQVAKLNPPEALAAKLEV
KHCTDQISFKKRLSLKKSWWK

0930427-114401

FIGURE 179

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGG
TGAAGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTG
GAGCAGATCCGTGGGCTGCAGACCCCGCCCCAGTGCCCTCTCCCCCTGCAGCCCTGCCCCCTC
GAACTGTGACATGGGAGAGAGTGACCCTGGCCCTTCTCCTACTGGCAGGCCTGACTGCCTTGG
AAGCCAATGACCCATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAAACCTGCAG
CTGAGCGGACTGATCTGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGG
CAAATGCAAATACAAGAGCAGCCAGAAGCAGCACAGTCCTGTACCTGAGAAGGCCATCCAC
TCATCACTCCAGGCTCTGCCACTACTTGCTTGAGCACAGGACTGGCCTCCAGGGATGGCCTGA
AGCCTAACACTGGCCCCCAGCACCTCCTCCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTC
TCTCCAAGGGCAGGCTGTTAGGCCCTTTCTGATCAGGAGGCTTCTTTATGAATTAACTCG
CCCCACCACCCCTCA

FIGURE 180

MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAAGIAAVLSGKCK
YKSSQKQHSPVPEKAIPILITPGSATTC

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FIGURE 181

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGG**ATG**TCGCTGCTGAGCCTGCC
TGGCTGGGCTCAGACCGGTGGCAATGTCCCATGGCTACTCTGCTGCTGGTTGTGGGCTC
CTGGCTACTCGCCCGCATCCTGGCTTGGACCTATGCCTTCTATAACAAGTCCCGCCGGCTCC
AGTGTTCCTCCACAGCCCCAAACGGAAC**TGG**TTTTGGGGTCACTGGGCTGATCACTCCT
ACAGAGGAGGGCTTGAAGGACTCGACCCAGATGTCGGCCACCTATTCCAGGGCTTTACGGT
ATGGCTGGGTCCCATCATCCCTTTCATCGTTTTATGCCACCTTGACACCATCCGGTCTATCA
CCAATGCCTCAGTGCCTATTGCACCCAAGGATAATCTCTTCATCAGGTTCTTGAAGCCCTGG
CTGGGAGAAGGGATACTGCTGAGTGGCGGTGACAAGTGAGCGCCACCCTCGGATGCTGAC
GCCCGCTTCCATTCCAACATCCTGAAGTCTATATAACGATCTTCAACAAGAGTGCAAAACA
TCATGCTTGACAAGTGGCAGCACCTGGCCTCAGAGGGCAGCAGTCGCTGGACATGTTTGAG
CATCATCAGCTCATGACCTTGGACAGCTACAGAAATGCATCTTCAGCTTTGACAGCCATTG
TCAGGAGAGGCCCATGGAATATATTGCCACCATTCTGGAGTCTGAGCTGCTTGATAGCAAAA
GAAGCCAGCATATCCTCCAGACCATGGAC**TTCT**GTAT**TAC**CT**TC**CCAT**GAC**GGCGGGCGC
TTCCACAGGGCTGCCGCTGGTGCATGACTTACAGACGCTGTCTATCCGGGAGCGGCGTGG
CACCTCCCCACTCAGGGTATTGATGATTTTTTCAAAGACAAAGCCAAAGTCCAAGACTTTGG
ATTTCAATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGGCATTGTCTAGATGAGGAT
ATAAGAGCAGAGGCTGACACCTTCATGTTTGGAGGCCATGACACCAGGCCAGTGGCCTCTC
CTGGTCTCTGTACAACCTTGCAGAGGACCCAGAATACCAGGAGCGCTGCCGACAGGAGGTGC
AAGAGCTTCTGAAGGACCGCGATCTCTAAAGAGATTGAATGGGACGACCTGGCCCAGCTGCC
TTCTGACCATGTGCTGAAGGAGAGCGCTGAGGTTACATCCCCAGCTCCCTTCATCTCCCG
ATGCTGCACCCAGGACATTGTTCTCCAGATGGCCGAGTCATCCCCAAAGGCATTACCTGCC
TCATCGATATTATAGGGGTCCATCACAACCCAAC**TGT**GTGGCCGGATCCTGAGGTCTACGAC
CCCTTCGGCTTTGACCCAGAGAACAGCAAGGGGAGGTCACTCTGGCTTTTATTCCTTTCTC
CGCAGGCGCCAGGAAC**TGC**ATCGGCAGGCGTTCGCCATGGCGGAGATGAAAGTGGTCTTG
CGTTGATGCTGCTGCACATTCGGTTCTCTGCGACGACCACTGAGCCCCGAGGAAGCTGGAA
TTGATCATCGCGCGCCAGGGCGGGCTTGGCTGCGGGTGAGAGCCCTGAATGTAGGCTTGCA
GTGACTTTCTGACCCATCCACCTGTTTTTTTGCAGATTGTCATGAATAAAACGCTGCTGCAAA

FIGURE 182

MSLLSLPWLGLRPVAMSPWLLLLLVGSWLLARILAWTYAFYNNCRRLQCFPPKRNWFWG
HLGLITPTEGLKDSTQMSATYSQGFTVWLGPIIPFIVLCHPDTIRSITNASAAIAPKDNLF
IRFLKPWLGEGILLSGGDKWSRHRMLTPAFHFNILKSYITIFNKSANIMLDKWQHASEGS
SRLDMFEHISLMTLDSLQKCIFSFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYY
LSHDGRRFHRACRLVHDFTDVIRERRRTLPTQGIDDDFKDKAKSKTLDIDVLLLSKDEDEG
KALSDEDIRAEADTFMFGGHDTTASGLSWVLYNLARHPEYQERCQEVQELLKDRDPKEIEW
DDLAQLPFLTMCVKESLRLHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVW
PDPEVYDFFRFDPENSKGRSPLAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHT
EPRRKLELIMRAEGGLWLRVEPLNVGLQ

FIGURE 183

CAACAGAAGCCAAGAAGGAAGCCGTCTATCTTGTGGCGATC**ATG**TATAAGCTGGCCTCCTGC
TGTTTGCTTTTCACAGGATTCTTAATCCTCTCTTATCTCTCCTCTCCTTGACTCCAGGGA
AATATCCTTTCAACTCTCAGCACCTCATGAAGACGCGCCTTAACCTCCGAGGAGCTAGAAA
GAGCTTCCCTTCTACAGATATTGCCAGAGATGCTGGGTGCAGAAAAGAGGGGATATTCTCAGG
AAAGCAGACTCAAGTACCAACATTTTAAACCAAGAGGAAATTTGAGAAAGTTTCAGGATTT
CTCTGGACAAGATCCTAACATTTTACTGAGTCATCTTTTGCCAGAATCTGAAAACCATACA
AGAAACGTGAGACTCCTGATTGCTTCTGGAAATACTGTGT**TGA**AGTGAAATAAGCATCTGT
TAGTCAGCTCAGAAACCCCATCTTAGAATATGAAAAATAACACAATGCTTGATTTGAAAC
AGTGTGGAGAAAACTAGGCAAACTACACCCTGTTTCATTGTTACCTGGAAAATAAATCCTCT
ATGTTTGCACAAAAAAAAAAAAAA

FIGURE 184

MYKLASCCLLFTGFLNPLLSLPLLDREISFQLSAPHEDARLTPEELERASLLQILPEMLGA
ERGDILRKADSSSTNIFNPRGNLRKFQDFSGQDPNILLSHLLARIWKPYKKRETPDCFWKYCV

FIGURE 185

GAACATTTTtagTtCCCAAGGAATGTACATCAGCCCCACGGAAGCTAGGCCACCTCTGGGAT
 GGGGTTGCTGGTTTAAACAAACGCCAGTCATCCTATATAAGGACCTGACAGCCACCAGGCA
 CCACCTCCGCCAGGAAGTGCAGGCCCCACCTGTCTGCAACCCAGCTGAGGCCATGCCCTCCCC
 AGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGGCCATGGCAGGCT
 CCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGCAGAGAAAGGAGTCGAAGAAGCCACCA
 GCCAAGCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCCGCCCCGGAAGATGGAGGTCAAGCAGA
 AGGGGCAGAGGATGAACTGGAAGTCCGGTTCAACGCCCCCTTTGATGTTGGAATCAAGCTGT
 CAGGGGTTCAGTACCAGCAGCACAGCCAGGCCCTGGGGAAGTTTCTTCAGGACATCCTCTGG
 GAAGAGGCCAAAGAGGCCCCAGCCGACAAGTGATCGCCCAAGCCTTACTCACCTCTCTCT
 AAGTTTAGAAGCGCTCATCTGGCTTTTCGCTTGCTTCTGCAGCAACTCCCACGACTGTTGTA
 CAAGCTCAGGAGGCGAATAAATGTTCAAACGTGA

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FIGURE 186

MPSPGTVCSELLLGLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPEDG
GQAEGAEDLEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADKO

05090427-131404

FIGURE 187

CGGCCACAGCTGGCATGCTCTGCCTGATCGCCATCCTGCTGTATGTCCTCGTCCAGTACCTC
 GTGAACCCCGGGGTGCTCCGCACGGACCCAGATGTCAAGAATATGAACACGTGGTGCTGT
 TCCTCCCCCTGTTCCCGGTGCAGGTGCAGACCCTGATAGTCGTGATCATCGGGATGCTCGTG
 CTCTGCTGGACTTTCTTGGCTTGGTGCACCTGGGCCAGCTGCTCATCTCCACATCTACCT
 GAGTATGTCCCCACCCTAAGCCCCGATCCCCCAAGGCTGGGTGGTCAGAGCTGTCATC
 TTACACCTCTACTTGAGTATGTCCCTAACCTGAGCCCCCAGCCTGGGGCCAGAGTCTTT
 GTCCCCCGTGTGCGCATGTGTTCAGGGTCAGCCTCTCCAGAAGTGAGATCATGGACAAAA
 GGGCAAATCACAGGAAGAAATTAAATCCATGAGGACCCAGCAGGCCAGCAAGAAGCTGAAC
 TCACGCCGAGACCTGCAGGAGTGGTGCCAGGTGCTTGAAGTAACAAGTTTAAAAATGTTCAGA
 GACAATGGAATGGAATCTATTAGGCAAGAACAGGACATTATGAAATAAGGACAGGTGGACTT
 CCAAAAACACAAGTAGAAATTCTAACAAATGAAATATATTACAGGCAGGTACCCACTAACCA
 AACAACTGAAGCGAGAGCTGTGGTCTTGCTTGGTCTCACAGTGGGCACAGCGGTAGGCGGT
 AGTCATGTTGCTGAACGACGGAGGGTAAACTCCCAGCCCCAAGAAAACCTGTGTTGGAAGT
 AACAAACACCTCCCTGCTCCTGGCACCCAGCCGTTTTGGTCTATGGTGGGCCAGCTGCAAGCG
 TCTTCATTCTCTGGGCAGTGGTGGCCCCGAGGCTGTGGCCTCTCAGGGGGTTCTGTGGAC
 ACGGGCAGCAGAGTGTGTCCAGGCCAGCCCCAAGAATGCCCTGCTCCTGACAGCTTGGCCA
 ACCCTTGCTCAGGCAGAGGGAGTTGGTGGGTGAGGCTCTGGGCTCACCTCCATCTCCAGA
 GCATCCCCCTGCCTGCAGTTGTGGCAAGAAGCCAGCTCAGAATGAACACACCCACCAAGA
 GCCTCCTTGTTCATAACCACAGGTTACCCCTACAAACCACTGTCCACACAACCCTGGGGAT
 GTTTTAAACACACACCTCTAACGCATATCTTACAGTCACTGTTGTCTTGCCTGAGGGTTGA
 ATTTTTTTTAAATGAAAGTGCAATGAAAATCACTGGATTAAATCCTACGGACACAGAGCTGAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 188

MNTWLLFLPLFPVQVQTLIVVIIIGMLVLLDFLGLVHLGQLLI FHIYLSMSPTLS PRSPQGW
VVRAAHLTPLEYPNPEPPTPGARVFVPRVRMCSGSASPRSEIMDKKGKSQEEIKSMRTQQ
AQQEAE LTPRPAGV VPGA

09990427-111491

FIGURE 189

GGAGTGCAGATGGCATCCTTCGGTTCTTCCAGACAAGCTGCAAGACGCTGACC**ATG**GCCAAAG
 ATGGAGCTCTCGAAGGCCTTCTCTGGCCAGCGGACACTCCTATCTGCCATCCTCAGCATGCT
 ATCACTCAGCTTCTCCACAACATCCCTGCTCAGCAACTACTGGTTTGTGGGCACACAGAAGG
 TGCCCAAGCCCTGTGCGAGAAAGGTCTGGCAGCCAAGTGCTTTGACATGCCAGTGTCCCTGA
 GATGGAGATACCAACACATCCACCCAGGAGGTGGTACAATAACAATGCGAGACTGGGGATGA
 CCGGTTCTCCTTCCGGAGCTTCCGGAGTGGCATGTGGCTATCCTGTGAGGAAACTGTGGAAG
 AACCAGGGGAGAGGTGCCGAAGTTTCATTGAACCTTACACCACCAGCCAAGAGAGGTGAGAAA
 GGACTACTGGAATTTGCCACGTTGCAAGGCCCATGTCACCCCACTCTCCGATTGTGGAGGAA
 GCGGTTGATGGAGAAGGCTTCCCTCCCCTCCCCTCCCCTGGGGCTTTGTGGCAAAAATCCTA
 TGGTTATCCCTGGGAACGAGATCACCTACATCGGACTTCAATTCATCAGCTTCCTCCTGCT
 ACTAACAGACTTGCTACTACTGGGAACCTGCCTGTGGGCTCAAACCTGAGCGCCTTTGCTG
 CTGTTTCTCTGTCTGTCAAGTCTCCTGGGGATGGTGGCCACATGATGTATTACAAAGTC
 TTCCAAGCGACTGTCAACTTGGGTCCAGAAGACTGGAGACCACATGTTTGAATTATGGCTG
 GGCTTCTACATGGCTGGCTCTCCTTACCTGCTGCATGGCGTCGGCTGTCAACACCTTCA
 ACACGTACACCAGGATGGTGTGGAGTTCAAGTGCAAGCA**TAG**TAAAGAGCTTCAAGGAAAAC
 CCGAAGTGCCTACCACATCACCATCAGTGTTTCCCTCGCGGCTGTCAAGTGCAGCCCCAC
 CGTGGGTCTTTGACCAGCTACCACCAGTATCATAATCAGCCCATCCACTCTGTCTCTGAGG
 GAGTCGACTTCTACTCCGAGCTGCGGAACAAGGGATTTCAAAGAGGGGGCCAGCCAGGAGCTG
 AAAGAAGCAGTTAGGTCATCTGTAGAGGAAGAGCAGTGTTAGGAGTTAAGCGGGTTTGGGGA
 GTAGGCTTGAGCCCTACCTTACACGCTGTGCTGATTATCAACATGTGCTTAAGCCAACATCCG
 TCTCTTGAGCATGGTTTTTAGAGGCTACGAATAAGGCTATGAATAAGGGTTATCTTTAAGTC
 CTAAGGGATTCTGGGTGCCACTGCTCTCTTTTCTCTACAGCTCCATCTTGTTTCACCCAC
 CCCACATCTCACACATCCAGAATTCCCTTCTTTACTGATAGTTTCTGTGCCAGGTTCTGGGC
 TAAACCATGGAGATAAAAAAGAAGAGTAAAATACACTTCCCGACCTTAAGGATCTGAAA

FIGURE 190

MAKMELSKAFSGQRTLLSAILSMSLSFSSTTSLLSNYWFVGTQKVPKPLCEKGLAAKCFDMP
VSLDGDNTNSTQEYVQYNWETGDDRFSSFRSFRSGMWLSCEETVEEPGERCRSFIELTPPAKR
GEKGLLEFATLQGPCHPTLRFGGKRLMEKASLPSPPLGLCGKNPMVIPGNADHLHRTSIHQ
PPATNRLATHWEPCLWAQTERLCCCFLCPVRSPGDGGPHDVFTSLPSCQLGSRRLLETTCLE
LWLGLLHGLALLHLLHGVGCHHLQHVVHQDGAGVQVQA

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FIGURE 191

AAC TGAAGGAAAGAAAGAGAAAGGTGACGCTTTGGCCCA**GATG**TGGTTACCCCTTGGTCTCTGT
TCTTTATGTCTTTCTCCTCTTCTTATTCTGTGTCATCTCCCTCACTTAAGTCTCAGGCGCTGTCA
GCAGCTCCTGTGGACATTGCCATCCCTCTGGTAGCCTTCAGAGCAAAACAGGACAACCTATG
TTATGGATGTTTCCACCAACCAGGGTAGTGGCATGGAGACCCGTAACCATCTGTGCTTCTGT
GATCTCTATGACAGAGCCACTTCTCCACCTCTGAAATGTTCCCTGCTCTGAAATCTGGCATG
AGATGGCACAGGTGACCACGCAGAAGCCACCAGAATCTTGCCTGCCCTATTCTCTCTCCAA
GTCTGTTCTCTTATTGTCAACCTCAGCACAAACAGGCTGGCGCAATGGCATTACAGAGAAAG
CAATCTGTGTGGTAGTGGGCAGATTACCATGCAAGCCCCAGGAGAATGGAGGAGCTTTGT
AGCCACCTCCCTGTGACGCAGTATTAAATGTGCCCTTCCCCCTGCCCGCCGCTAGATTGAG
GACATTGCCCCCTGTGTGCCACCAAAACCAGGACTTTCCCTTGGCTTGGCATCCCTGGCTCT
CTCCTGGTACCCAGCAAGACGCTGTGTTCCAGGGCAGTGTAGCATCTTTCAAGCTCCGTTACT
ATGGCGATGGCCATGATGTTACAATCCCACCTTGCTGAATAATCAAGTGGGAAGGGGAAGCA
GAGGGAAATGGGGCCATGTGAATGCAGCTGCTCTGTTCTCCCTACCTGAGGAAAAACAAA
GGGAAGCAACAGGAACTCTGCAACTGGTTTTTATCGGAAAGATCATCCTGCCTGCAGATGC
TGTTGAAGGGGCACAAGAAATGTAGCTGGAGAAGATTGATGAAAGTCAGGTTGTGTAAGGAA
ATAGAACAGTCTGCTGGGAGTCAGACCTGGAATTTCTGATTCCAACTCTTTATTACTTTGGG
AAGTCACTCAGCTCCCCGTAGGCATCTCCAGGTGACGGAACCCAGTGTATTACCTGCTGG
AACCAAGGAAACTAACATGTAGGTTTACTAGTGTGAATACCCCAATGGTTTCTCCAATTATGCC
CATGGCACCAAAACAATAAAACAAAATTTCTTAACACTGAAA

FIGURE 192

MWLPGLLSLCLSPILSSPSLKSQACQQLLWTLPSPPLVAFRANRTTYVMDVSTNQGSME
HRNHLCFCDLYDRATSPPLKCSLL

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FIGURE 193

GTAGCGCGTCTTGGGTCTCCGGCTGCCGCTGCTGCCGCCGCCGCTCGGGTCTGGAGCCAGGAGCGACGTCA
 CCGC**ATG**CAGGCGATCAAAGCTTTGATAGTATTTGCTCTTTGGAGGACAAATCGGACTGATGTTTTGATGCTT
 GGATGTGCCCTTCCAATAACAAACAATACTGCCCTCTTTGTTCTATTTTTTACATCCTTTCACTATTTCC
 ATACTGCATAGCAAGAAGATTAGTGGATGATACAGATGCTATGAGTAAACGCTTGTAAAGAACTTGGCATCTTTC
 TTAACAAGGGGCAATTGTCGTGCAGCTTTTGGACTCCCTATTGTATTTGCCAGAGCAGCATCTGATTGAGTGGGGA
 GCTTGTGCACCTGTTCTACAGGAAACACAGTCATCTTTGCAACTATACTAGGCTTTTCTTGGTCTTTGGGAAG
 CAATGACGACTTCACTGGCAGCAGTGG**TGA**AAAGAAATTAAGTGAACATTTGTCAAATGGACTTCCGTGCATT
 GTTGGCCATTACGCGACACAGGAGATGGGGCAGTTAATGCTGAATGGTATAGCAAGCCTCTTGGGGGATTTTA
 GGTGCTCCCTTCTCACTTTATTGTAAGCATACTATTTACAGAGACTTGTCTGAAGGATTAAGAGGATTTTCT
 CTTTGGAAAAGCTTGACTGATTTACACTTATCTATAGTATGCTTTTGTGGTCTCTGCTGAATTTAAATAT
 TTATGTGTTTTCTGTAGGTTGATTTTTTGGAAATCAATATGCAATGTTAAACACTTTTTTAATGTAATCA
 TTGCAATGGTTAGGAATTCAGAAATCCGCCGGCTTATTACTGGTCAAGTACATCTTTCTCTTAAATATT
 TAGCCTCCATTATTACAAAAAATATAAAAAAAGTTTTCACTAGTCAGGATGACATCACTCCCAATGTTATG
 CAGACATACAGACGGTTGGCATACTTATAGACTGTATACTCAGTGCAATATAGCTGCATTTATACCTCAGAG
 GGGCCAAGTGTTAATGCCATGCCCTCCGTTAAGGGTTGTGGTTTTACTGGTAGACAGATGTTTTGGGATTG
 AAGTAAGGGTGAAAAACATTTTGAGATAAGGTTTTATTATGTTTATTATTGTAGATGAGTTGCAATGT
 AAAAATTTTATGGAATTGCTACAGAGGAGTGCTTTTCTCTCAATTGTTAGAAGAAATTTATGTTAACTTTA
 AACCTTTTCATGTTTTACCTGTTAAATGGACATACATGGAACCACTACTGATGAGGGACAGTTGATGTTTGC
 ATCATATATGCCAGAAAAACCTTCTCTGCTTCCCTCTTTGACTTATTGGTATGTTGTATATATTACATAAAA
 TAACTTTTCAATATAGTTTAAATAACACTTAGAAGTGTTACTTACCTGGAAAATTAATGCTATGCCGTACATT
 CAGAGTGCCCTCCCTGCAAGGCCCTGCCATGATTAAACAAGTAACTTGTAGTCTACAGATATTCATGCA
 TTAACAGTTTAAAGATTAGACCATGGTAAATAGTAGTCTTATTCTCTAAGGTATATCATATGTAATTTAAAG
 TATTTTTAAGACAAGTTTCTGTATACCTCTGAAGCTTTTGTATTGAGTTCATGATCATGATAGATCTGCTGTT
 CCTTTAAAGGCATTTGTTGTGAGTTAATGCAAGTAGCCAGTCCAGCTATATAGCAGCTTCAGAAACAT
 ACCTGACCAAAAAATTCOCAGTAACCAAGCATGATCAATTTATAGTGGTCGTTTACATCTAATAATTAACGGA
 CTTTTTTCAGGAGTGGGTTATAAAAAATTTCAAGTTGCTGACAGTATTTTGTAAAGATTTGTTTGTATG
 TTTATTAGTATTTATTCTCAAGAAAAATGGGAATAAATTTGGGATTGTTCTAGCTTTTTACTAAAGATGCCTAA
 AGCCACAGGTTTTATTGCTTAACCTTAAGCCATGACPTTATAGATATGAGATGACGGGAAGCAGGACGAATATCG
 GCGTGTGGCTGGAGCCTCCCATCTGGAGGCTGAAAGTGGCTTGTGGTATATAAATTTAGATTTCAGAGGAA
 GGTGCAGGTACACATGAGTTAGAGAGCTGGTGAAGAGTGGGAAGTCTTTGTGCTGTGATCTACTGGAGCTT
 TTTTTTCCAGGAAGTGCATTTCTCGTCTTCCCTATTTCGATTTCTGGAATGTCAGTGACAGTGCATGCTGCTG
 TTTTATCCACTTGGCCACAGACTTTTCTAACAGCTGCGTATTTTCTATATCTAATTCATTTGGCAGCATG
 GTGCTCTTGACCTGTATCTAGCTTGCATAGTGTCTGCTGATTTCTAGGCTAGTTACTTGAATATGAAT
 TTCCATAGAAATATGACTGATACACATTACCATTTCTATGGAAGAAAACCTTTGATGATGAACAATAA
 AGATTTTAAATATCTATTTTAAAAAATAA

FIGURE 194

MAGIKALISLSFSGAIGLMFLMLGCALPIYNKYWLFVLFFYILSPIPYCIARRLVDDTDAM
SNACKELAIFLTGTGIVVSAFGLPIVFARAHLEWGACALVLTGNTVIFATILGFFLVFGSND
DFSWQQW

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[illegible]

FIGURE 196

MDFLLLGLCLYWLLRRPSGVVLCLLGACFQMLPAAPSGCFQLCRCEGRLLYCEALNLTEAPH
NLSGLLGLSLRYNSLSELRAQFTGLMQLTWLYLDHNNHICSVQGDAFQKLRRVKELTLSSNQ
ITQLPNTTFRPMPNLRSDLSYNKLQALAPDLFHGLRKLTTLHMRANA IQFVPVRIFQDCRS
LKFLDIGYNQLKSLARNSFAGLFKLTLEHLEHNDLVKVNFAHFPRLISLHSLCLRRNKVAIV
VSSLDWVWNLEKMDLSGNEI EYMEPHVFETVPHLQSLQLDSNRLTYIEPRILNSWKSLSITSIT
LAGNLWDCGRNVICALASWLSNFGQRYDGNLQCASPEYAQGEDVLDVYAFHLCEDGA EPTSG
HLLSAVTNRSDLGPPASSATTLADGGEGQHDGTFEPATVALPGGEHAENAVQIHKVVTGTMA
LIFSFLIVVLVLYVSWKCFPASLRQLRQCFVTQRRKQKQKQTMHQMAAMSAQEYYVDYKPNH
IEGALVIINEYGSCTCHQQPARECEV

FIGURE 197

GTGCAAGGAGCCGAGGCGAGATGGGCGTCCTGGGCCGGGTCTGCTGTGGCTGCAGCTCTGC
 GCACTGACCCAGGCGGTCTCCAAACTCTGGGTCCCCAACACGGACTTCGACGTCGCAGCCAA
 CTGGAGCCAGAACCGGACCCCGTGCGCCGGCGGCGCCGTTGAGTTCCCGGCGGACAAGATGG
 TGTCAGTCCTGGTGCAAGAAGGTCACGCCGTCTCAGACATGCTCCTGCCGCTGGATGGGGAA
 CTCGTCTTGGCTTCAGGAGCCGGATTGCGCGTCTCAGACGTGGGCTCGCACCTGGACTGTGG
 CGCGGGCGAACCTGCCGTCTTCCGCGACTCTGACCGCTTCTCCTGGCATGACCCGCACCTGT
 GGCGCTCTGGGGACGAGGCACCTGGCCTCTTCTTCGTGGACGCCGAGCGCTGCCCTGCCGC
 CACGACGACGTCTTCTTCCGCCTAGTGCCTCCTTCCGCGTGGGGCTCGGCCCTGGCGCTAG
 CCCCCTGCGTGTCCGAGCATCTCGGCTCTGGGCCGGACGTTACGCGCGACGAGGACCTGG
 CTGTTTTCTGGCGTCCCGCGCGGGCCGCTACGCTTCCACGGGCCGGGCGCGCTGAGCGTG
 GGCCCCGAGGACTGCGCGGACCCGTGCGGCTGCGTCTGCGGCAACGCGAGGCGCAGCCGTG
 GATCTGCGCGGCCCTGCTCCAGCCCCT

FIGURE 198

MGVLGRVLLWLQLCALTQAVSKLWVPNTDFDVAANWSQNRTPCAGGAVEFPADKMVSVLVQE
GHAVSDMLLPLDGELVLASGAGFGVSDVGSHLDCGAGEPAVFRSDRFSWHDPHLWRSGDEA
PGLFFVDAERVPCRHDDVFFPPSASFRVGLGPGASPVVRVSISALGRFTTRDEDLAVFLASR
AGRLRFHGPGALSGPEDCADPSGVCVGNAEAQPWICAALLQP

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[illegible]

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FIGURE 200

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGALIFCIIQSLALTWYLSFIP
FARDAVKKCFVCLA

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FIGURE 201

TTGAGCGCAGGTGAGCTCCTGCGCGTTCCGGGGGGCGTTCCCTCCAGTCAACCTCCCGCGGTACCCGCGCGCGCG
 CCGAGGGGAGTCTCCTCCAGACCTTCCCTCCCGTTGCTCCAACTAATACGAGTGAACGGATCGCTGCGAGGGGT
 GGGGAGAAAAATTAGGGGGGAGAAAGGACAGAGAGAGCACTACCATCCATAGCCAGATAGATTCTTACACTG
 AACTGATCAAGTACTTTGAAATATGACTTCGAAATTTATCTTGGTGTCCCTTCATACTTGGTGCAGTGAAGTCTTC
 AACCACTTTTCTCTCCAACTAGACCAGCAAAAGGTTCTACTAGTTCCTTTGATGGATTCCGTTGGGATTTACT
 TATATTAAGGTTCCACGCCCATTTTCATATATATGAAATATGGTGTTCAGTGAAGCAAGTTACTCATATGTT
 TTTTATTAACAACTACCTTAACCATTTACTTTGGTAAGTGGCCTCTTCGACAGAGATCATGGGATTTGTGTC
 AAATGATATGTTTGATCCTATTTCGGAACAAATCTTCTCCTTGGATCACATGAATATTTATGATTCCAAGTTT
 GGAAGAGAGCGACCAATATGGATCACAAACGAGGGGAGGACATAGTGGTGCAGCCATGTGCGCCGGA
 ACAGATGTAAAAATACATAAGCGCTTCCCTACTCATATGCTTACATGAGTGAAGTTCATTTGAAGATAG
 AGTTGCCAAATTTGTGAATGTTTACGTCAAAGAGCCCATTAATCTTGGTCTTCTATTGGGAAGACCTG
 ATGACATGGGCCACCTTTGGGACCTGACAGTCCGCTCATGGGGCTGTCTTTCAGATATTGACAGAAGTTA
 GGATATCTCATACAAATGCTGAAAAGGCAAGTTGTGGAACACTCTGAACCTAATCATCAAGTGATCATGG
 AATGACGCGAGTCTCTGAGGAAAGGTTAATAGAATTTGACCACTGACCTGGATAAAGACCATATACCTGATTG
 ATCAATCTCCAGTAGCAGCCATCTTGCCAAAGAGAGTTAAATTTGATGAAGTCTATGAAGCACTAATCACGCT
 CATCCTAATCTTACTGTTTACAAAAAGAGAGCTTCCAGAAAGGTGGCATTACAAATACAACAGTCGAATTCA
 ACCAATCATAGCAGTGGCTGATGAAGGGTGGCAGATTTACAGATTAAGTCAGTACTTCTGTTAGGCAACC
 ACGGTTACGATAATGCGTTAGCAGATATGCATCCAATATTTTACCCCATGGTCTGCTTCAGAAAGAAATTC
 TCAAAAGAGCCATGAATCCACAGATTTGTACCACTACTATGGCCACTCCTCAATATCACTGCCATGCCACA
 CAATGGATCATTTGGAATGTCCAGGATCTGCTCAATTCAGCAATGCCAAGGGTGGTCCCTTATACACAGAGTA
 CTATACTCCTCCTGGTAGTGTTAAACCAGCAGAAATAGACCAAGAGGGGTATACCTCTATTTCATAGGGGTC
 TCTCTTGGCAGCATTTATAGTGATTGATTTTGTAAATTTTCAATTAAGCATTTTTCACAGTCAAAATCTGTC
 CTTACAAGATATGCATGCTGAATAGCTCAACATTATACAGCGTAAATGTTACTTGAAGTGGATTTGCTA
 TTGAAGTGGAGATCCATAATATGTCACTGTTTAAAGGTTTCAAAATTCGGGAACCACTTCCAAACATCTGC
 AGAAACCATTAAGCAGTTACATATTTAGGTATACACACACACACACACATACACACACACGGGCCAAA
 ATACTTACACCTGCAAGGAATAAAGATGTGAGATATGTCTCCTTGTCTACTGTAGCATAGGGATAGATAAG
 ATCTGCTTTATTTGGACTTGGCGCAGATAATGTATATTTAGCACTTTCACATATGAAAGTACCTTATAT
 ATTGCACTTTAAATTTCTCTCTGTGGGTACTTTAATTTGAATGCATTTATGGCAGTTATGCTTATAAC
 TTGATTGAAATGACACTTTTTCACCCATGTACAGAAATACTGTTACGCATTTGTCAAACTGAAGGAAAT
 TCTAATTAATCCGAAATGAACATAGAAATCTATCTCCATAAATGAGAGAAGAGAAGGTGATAAGTGTGA
 AAATTAATGTATAACCTTGAACCTTCAATTTTGGAGATGATTTCCCAACAGCAGAAATGCAACTGTGGGCAT
 TTTCTTGTCTTATTTCTTTCCAGAGACGTGGTTTTCAATTTATTTTCCCTCAAAGAGAGTCAAACTACTGACAG
 ATTCTGCTCAATATATTTGTTCTGTCAATAAATATTTGATTTCCTGATGAGTCAATATTTACTGTGATTTTCA
 TAATAATGAACACCATCAATATCTTTCTCTATATAGTTAGCAATGGCCTGAATGAAAGCAACCGGCA
 CCATCTCAGCAATGTTTCTCTGTTTGTATATTTGCTCCTTTGAAATTAATCACTATTAATCACTTAA
 AAATCAAATGGATAAAAA

FIGURE 202

MTSKFILVSFILAALSSTTFSLQLDQQKVLVVSFDGFRWDYLYKVPTPHFHYIMKYGVHVK
 QVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEETPIW
 ITNQRAGHTSGAAMWPGTDVKIHKRFPPTHYMPYNESVSFEDRVAKIVIEWETSKEPINLGLLY
 WEDFDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTLNLIITSDHGMTQCSEER
 LIELDQYLDKDHYTELDQSPVAAILPKEGKFDEVYEALTHAHPNLTVYKKEDVPERWHYKYN
 SRIQPIIAVADEGWHLQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFRKNFSKEAMNSTD
 LYPILLCHLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSVKPAEYDQEGSYPYF
 IGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

Signal Peptide:

amino acids 1-22

Transmembrane Domain:

amino acids 429-452

N-glycosylation sites:

amino acids 101-104, 158-161, 292-295, 329-332, 362-365, 369-372, 382-385, 389-392

Somatomedin B Domain:

amino acids 69-85

Sulfatase protein Region:

amino acids 212-241

FIGURE 203

GGATTTTGTGATCCGCGATTTCGCTCCACGGGCGGGACCTTTGTAAGTGCGGGAGGCCAG
 GACAGGCCACCCCTGCGGGGCGGGAGGCAGCCGGGGTGAAGGAGGTGAAGAAACCAAGACGC
 AGAGAGGCCAAGCCCTTGCCCTTGGGTACACAGCCAAAGGAGGCAGAGCCAGAAGTACAA
 CCAGATCCAGAGGCAACAGGGAC**ATG**CCACCTGGGACGAAAAGGCAGTCAACCGCAGGGCC
 AAGGTGGCTCCCGCTGAGAGGATGAGCAAGTCTTAAGGCACTTACGGTCGTGGGAGACGA
 CTACCATGCTGGAACATCAACTACAAGAAATGGGAGAATGAAGAGGAGGAGGAGGAGGAGG
 AGCAGCCACCACCCACACCACTCTCAGGCGAGGAAGGCAGAGCTGCAGCCCTGACGTGCC
 CCTGCCCTGGCCCCGACCCAGGGCCCCCTTGACTTCAGGGGCATGTTGAGGAACTGTT
 CAGCTCCACAGGTTTCAGGTCATCATCATCTGCTTGGTGGTCTGGATGCCCTCCTGGTGC
 TTGCTGAGCTCATCTGGACCTGAAGATCATCCAGCCCGACAAGAATAACTATGCTGCCATG
 GTATTCACACTACATGAGCATCACCATCTTGGTCTTTTTATGATGGAGATCATCTTTAAATT
 ATTTGTCTTCCGCTGAGTTCCTTACCACAAGTTTGAGATCCTGGATGCCCGTCGTGGTGG
 TGGTCTCATTCATCTGGACATTGCTCCTCTGTTCCAGGAGCACCAGTTTGAGGCTCTGGGC
 CTGCTGATTCTGCTCCGGCTGTGGCGGGTGGCCCGGATCATCAATGGGATTATCATCTCAGT
 TAAGACACGTTTCAGAACGGCAACTCTTAAGGTTAAAACAGATGAATGTACAATTGGCCGCCA
 AGATTCAACACCTTGAGTTCAGCTGCTCTGAGAAGCCCTGGAC**TGA**TGAGTTTGCTGTATC
 AACCTGTAAGGAGAAGCTCTCTCCGGATGGCTATGGGAATGAAAGAATCCGACTTCTACTCT
 CACACAGCCACCGTGAAAGTCTTGAGTAAAATGTGCTGTGTACAGAAGAGAGAGAAGGAAG
 CAGGCTGGCATGTTCACTGGGCTGGTGTACGACAGAGAACCTGCAGTCACTGGCCAGTTA
 TCACTTCAGATTACAAATCACACAGAGCATCTGCCTGTTTTCAATCACAAGAGAACAAAACC
 AAAATCTATAAAGATATTCTGAAAAATATGACAGAATTTGACAAATAAAGCATAAACGTGTA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 205

CGGCTCGAGCTCGAGCCGAATCGGCTCGAGGGGCAGTGGAGCACCCAGCAGGCCGCCAACAT
 GCTCTGTCTGTGCCTGTACGTGCCGGTTCATCGGGGAAGCCAGACCGAGTTCCAGTACTTTG
 AGTCGAAGGGGGTCCCTGCCGAGCTGAAGTCCATTTTCAAGCTCAGTGTCTTCATCCCCCTCC
 CAGGAATTTCTCCACCTACCGCAGTGGAAAGCAGAAAAATGTACAAGCTGGAGATAAGGACCT
 TGAATGGGCAGCTAGACTTTGAAGAAATTTGTCCATTATCTCCAAGATCATGAGAAGAAGCTGA
 GCCTGGTGTTTAAGATTTTGGACAAAAAAGAAATGATGGACGCATTTGACGCCGAGGAGATCATG
 CAGTCCCTGCGGGGACTTGGGAGTCAAGATATCTGAAACAGCAGGCAGAAAAAATTTCTCAAGAG
 CATGGATAAAAAACGGCACCATGACCATCGACTGGAACGAGTGGAGAGACTACCACTCTCTCC
 ACCCGTGGAAAAACATCCCCGAGATCATCTCTACTGGAAGCATTCACAGTCTTTGATGTG
 GGTGAGAAATCTAACGGTCCCGGATGAGTTACAGTGGAGGAGAGGCAGACGGGGATGTGGT
 GAGACACCTGTGTGGCAGGAGGTGGGGCAGGGGCGGTATCCAGAACCTGCAACGGCCCCCTGG
 ACAGGCTCAAGGTGCTCATGACAGTCCATGCTTCCCGCAGCAACAACATGGGCATCGTTGGT
 GCCTTCACTCAGATGATTGAGAGAGGAGGGGCCAGGTCACTCTGGCGGGGCAATGGCATCAA
 GCTCTCAAAATTTGCCCCGAATCAGCCATCAAAATTCATGGCCATGAGCAGATCAACGCC
 TTGTTGTAGTGACAGGAGAGACTCTGAGGATTCACGAGAGGCTTTGTGGCAGGGTCTTGGCA
 GGGCCATCGCCACAGCAGCATCTACCCAAATGGAGGTCTGAAGACCCGGATGGCGCTGCG
 GAGACAGGGCCAGTACTCAGGAATGCTGGACTGCGCCAGGAGGATCTGGCCAGAGAGGGGG
 TGGCGGCTTCTACAAAGGCTATGTCCCCAACATGCTGGGCATCATCCCCATGCGCGCATC
 GACTTGCAGTCTACGAGACGCTCAAGAAATGCTGGCTGCAGCAGTATCGAGTGAACAGCGC
 CCAGCTACCGGCTGTGTTGTGCTCTGGGCTGTGGCACCATGTGACAGTCTTGTGGCCAGCTGG
 CCAGCTACCGCTTGGCCCTAGTCAGGACCCGGATGACAGGCCAAGGCTCTATTGAGGGCGCT
 GCGAGGTGACCATGACGAGCCTCTTCAAAATATCTCTCGGACAGAGGGGGCTCTCGGGCT
 CTACAGGGGGCTGGCCCCAATCTCATGAAGGTCACTCCAGCTGTGAGCATCAGCTACGTGG
 TCTACGAGAACTGAAGTACCCTGGCGTGCAGTGCCTGTCAGGGGGGAGGGGCCCGCC
 CGAGTGGACTCGCTGATCTGGGCGCGAGCTGGGGTGTGAGCCATCTCATTTCTGTAAT
 TGCCAACTAAGCTGTCTCGAGCCAAAGCTGTGA AAAACCTAGACGCACCCGACAGGGAGGT
 GGGGAGAGCTGGCAGGCCAGGGCTTGTCTGCTGACCCAGCAGACCCCTCTGTGTGTTCC
 AGCAGAGACCAAGCAGCATTTCTTAGGGTCCAGGCTCAGCAGGCTCCGGGCTCATATGTTAA
 GACGAGGACATTTCTGCACTGCTGCGCAATAGTGAGCTTGGAGGCTGGAGGCGGGCTTAGT
 TCTTTCATTTACCTTTGCAGCCAGCTGTTGGCCACGGCCCTGCCTCTGTGCTGCGGTGC
 ATCTCCTGTGCCCTCTGCTGCTGCTGTCTGCTGAGGTAAAGTGGGAGGAGGGCTACAG
 CCCACATTCACCCCTCGTCCAAATCCCATATCCATGATGAAAGTGAAGTCACTGCGCCT
 CCCAGGCTGACTTCCCACTACAGCATTTGACGCCAATTTGGCTGTGAAGGAAGAGGAAAG
 GATCTGGCTTTGTGCTCACTGGCATCTGAGCCCTGCTGATGGCTGGGGCTCTCGGGCATGCT
 TGGGAGTCAGGGGGCTCGGGCTGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
 TGGTGTCTGAGCTGGCTGGACCTTGCAGGATGGCCACCCACCTCAGAACCTGCTGCTGCT
 TCCCCATGTGGCATGAGGCGAGTGGAGCACCATGTTTGGGGCGAAGGCGAGCGGCTTTGT
 GTGTTCTGGGAGGGAAGGAAAGGTGTTGGAGGCTTAATATGACTGTTGGGAAAGAGGG
 TTTTGTCCAGAGGACAAGCCGACAAATGAGCGACTTCTGCTTCCAGAGGAAAGAGCGG
 GAGCAGGAGCTTGGCTGACTGCTCAGAGTCTGTGCTGAGCGCTTGGGGGTTTCTGTCCAAAC
 CCAGAGGGGCGCAGGCGGACGACCCACATTTCCATTTGTGCTACTGCTTGGAACTTATTT
 ATTTTGTATTTATTTGAACAGAGTTATGTCCTAACTATTTTATAGATTTGTTTAAATAA
 GCTTTGATTTTCAAAGTCTATTTTATTTATGATTTTGTGTTGATTTGACTTCCC
 AAGCCGCCCAAGTGGGATGGGAGGAGGAGGAGGAGGGGGGCTTGGGCCGCTGACGTCACAT
 TCTTCCAGAGAAATTTCTTTTGGGACTGGAAGCAGAAAGCGGCCAGGAGGCGAGCCGCTG
 GCTCTTTCTTTTGGCAGTTTGGGGAAGGGCTTGGCCCGAGCTTGGATTTTCAAGGTTTGA
 CTGGGGGCTGGAGAGAGAGGAGGAGAACCTCAATAACCTTGAAGTGGAAATCAGATTTTGA
 CTGCGCTGCGAGGGTTTCTTTATTTCACTCTTTTCTGATGTCAGGCTGAGGTTGAGGCTCT
 CACTGTGAAATTTGTGTTGGCGGGGCTGGAGGAGAGGTGGCGGGCTGGCTGCTGCTCTCC
 CAGCCTTCTGCTGCTGCTGCTTAAACATGCCGGCACTGGCGAGCTCAGCGTTGCACTTCC
 ATTCCACAGAATGACCTGATGAGGAAATCTCAATAGGATCAAGATCAATGCAAAAAT
 GTTATATATGAACATATACTGGAGTCTGCAAAAGCAAAATTAAGAAAGATTTGGACGTTAG
 AAGTTGTCAATTAAGACGCTTCTAATAAAGTTGTTCAAGCTGAAAAAATAAAAAA
 AA

FIGURE 206

MLCLCLYVPVIGEAQTEFQYFESKGLPAELKSIFKLSVFIPSQEFSTYRQWKQKIVQAGDKD
 LDGQLDFEEFVHYLQDHEKKRLVFKILDKKNDGRIDAQEIMQSLRDLGVKISEQQAEKILK
 SMDKNGTMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTVPDEFTVEERQTGMW
 WRHLVAGGGAGAVSRTCTAPLDRLKVLQMQVHASRSNNMGIVGGFTQMIREGGARSLWRNGI
 NVLKIAPESAIFMAYEQIKRLVGSDQETLRIHERLVAGSLAGAIQSSIYPMEVLKTRMAL
 RKTGQYSGMLDCARRILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNLQHYAVNS
 ADPGVFVLLACGTMSSTCGQLASYPLALVRTRMQAQASIEGAPEVTMSSLFKHILRTEGAFG
 LYRGLAPNFMKVIPAVSISYVVYENLKITLGVQSR

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domain:

amino acids 284-304, 339-360, 376-394

Mitochondrial energy transfer proteins signature.

amino acids 206-215, 300-309

N-glycosylation site.

amino acids 129-133, 169-173

Elongation Factor-hand calcium-binding protein.

amino acids 54-73, 85-104, 121-140

FIGURE 207

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCCAT
GGCTTCCCTGGGGCAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAG
 CAATTGCACATCATTTGGCTTTGGTATTTTCAGGGAGACACTCCATCACAGTCACTACTGTC
 GCCTCAGCTGGGAACATTGGGGAGGATGGAATCCTGAGCTGCACCTTTTGAACCTGACATCAA
 ACTTTCTGATATCGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTCCATGAGTTCA
 AAGAAGGCAAAGATGAGCTGTCGGAGCAGGATGAAATGTTTCAGAGGCCGACAGCAGTGTTT
 GCTGATCAAGTGATAGTTGGCAATGCCCTCTTTCGGGCTGAAAAACGTGCAACTCACAGATGC
 TGGCACCTACAATGTTATATCATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATA
 AAACCTGGAGCCTTCAGCATGCCGAAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTG
 CGGTGTGAGGCTCCCCGATGGTTCCCCAGCCACAGTGGTCTGGGCATCCCAAGTTGACCA
 GGGAGCCAACCTTCTCGGAAGTCTCCAATACCAGCTTTGAGCTGAACTCTGAGAATGTGACCA
 TGAAGGTTGTGTCTGTGCTCTACAATGTTACGATCAACAACACATACTCCTGTATGATTGAA
 AATGACATTGCCAAAGCAACAGGGGATATCAAAGTGACAGAATCGGAGATCAAAAGGCGGAG
 TCACCTACAGCTGCTAAACTCAAAGGCTTCTCTGTGTCTCTTCTTTCTTTGCCATCAGCT
 GGGCACTTCTGCCTCTCAGCCCTTACCTGATGCTAAAATAATGTGCCTTGGCCACAAAAAAG
 CATGCAAAGTCATTGTTACAACAGGGATCTACAGAACTATTTACCACCAGATATGACCTAG
 TTTTATATTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTGAGCAAAACAAGGCA
 AGAAACAAAAAGAAGCCAAAAGCAGAAGGCTCCAATATGAACAAGATAAATCTATCTTCAA
 GACATATTAGAAGTTGGGAAAATAATTCATGTGAAGTAGACAAGTGTGTTAAGAGTGATAAG
 TAAAATGCACGTGGAGACAAGTGCAATCCCCAGATCTCAGGGACCTCCCCCTGCCTGTCACCT
 GGGGAGTGAGAGGACAGGATAGTGATGTTCTTTGTCTCTGAATTTTTAGTTATATGTGCTG
 TAATGTTGCTCTGAGGAAGCCCTTGAAAGTCTATCCCAACATATCCACATCTTATATTC
 CAAATTAAGCTGTAGTATGTACCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAGG
 GGCGGCTGCATTTTAGTAATGGGTCAAATGATTCACTTTTTATGATGCTTCCAAAGGTGCCT
 TGGCTTCTCTTCCCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAA
 ACAGAGCAGTGGGGACACCGATTTTATAAATAAACTGAGCACCTTCTTTTTAAACAAAAA
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[illegible]

FIGURE 210

MAASLGQVLALVLVAALWGGTQPLLKRASAGLQRVHEPTWAQQLQEMKTLFLNTEYLMPFLLNQCSSLYYLTLASTDLTAVPICNSLAIIFTLIVGKALGEDIGGKRKLDYCECGTQLCGSRHTCVSSFPEPISPEWVRTRPFPILPFPLQLFCFLVAIRVPFPWTVVRKTEAGVWD

5

210/330
MAASLGQVLALVLVAALWGGTQPLLKRASAGLQRVHEPTWAQQLQEMKTLFLNTEYLMPFLLNQCSSLYYLTLASTDLTAVPICNSLAIIFTLIVGKALGEDIGGKRKLDYCECGTQLCGSRHTCVSSFPEPISPEWVRTRPFPILPFPLQLFCFLVAIRVPFPWTVVRKTEAGVWD

FIGURE 211

CTTCTGTAGGACAGTCACCCAGGCCAGATCCAGAAGCCTCTCTAGGCTCCAGCTTTCTCTGTG
 GAAGATGACAGCAATTATAGCAGGACCCTGCCAGGCTGTGCAAAAGATTCCGCAATAAACT
 TTGCCAGTGGGAAGTACCTAGTGAACGGCCTAAGATGCCACTTCTTCTCATGTCCCAGGCT
 TGAGGCCCTGTGGTCCCCATCCTTGGGAGAAAGTCAGTCCAGCACCATGAAGGGCATCCTCG
 TTGCTGGTATCACTGCAGTGCTTGTTGCAGCTGTAGAATCTCTGAGCTGCGTGCAGTGTAAAT
 TCATGGGAAAAATCCTGTGTCAACAGCATTGCCTCTGAATGTCCCTCACATGCCAACACCAG
 CTGTATCAGCTCCTCAGCCAGCTCCTCTCTAGAGACACCAGTCAGATTATACCAGAATATGT
 TCTGCTCAGCGGAGAACTGCAGTGAGGAGACACACATTACAGCCTTCACTGTCCACGTGTCT
 GCTGAAGAACACTTTTCATTTTGTAAAGCCAGTGCTGCCAAGGAAAGGAATGCAGCAACACCAG
 CGATGCCCTGGACCCCTCCCCTGAAGAACGTGTCCAGCAACGCAGAGTGCCCTGCTTGTTATG
 AATCTAATGGAACCTCCTGTCTGGGAAGCCCTGGAAATGCTATGAAGAAGAACAGTGTGTC
 TTTCTAGTTGCAGAACTTAAGAATGACATTGAGTCTAAGAGTCTCGTGCTGAAAGGCTGTTT
 CAACGTGAGTAACGCCACCTGTGAGTTCTGTCTGGTGAAACAAGACTCTTGGAGGAGTCA
 TCTTTCGAAAGTTTGAGTGTGCAAAATGTAAACAGCTTAACCCCCACGTCTGCACCAACCACCT
 TCCCACAACGTGGGCTCCAAAGCTTCCCTCTACCTCTTTGGCCCTTGCCAGCCTCCTTCTTCG
 GGGACTGCTGCCCCTGAGGTCTGGGGCTGCACTTTGCCCAGCACCCCATTTCTGCTTCTCTG
 AGGTCCAGAGCACCCCTGCGGTGCTGACACCCCTCTTTCCCTGCTCTGCCCCGTTTAACTGC
 CCAGTAAGTGGGAGTCACAGGTCTCCAGGCAATGCCGACAGCTGCCTTGTTCTTCAATTATTA
 AAGCACTGGTTCATTCACTGCCAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 212

MKGILVAGITAVLVAAVESLSCVQCNSWEKSCVNSIASECPSHANTSCISSASSSSLETPVR
LYQNMFCSAENCSEETHITAFTVHVSAEEHFHFVSQCCQGKECSNTSDALDPPLKNVSSNAE
CPACYESNGTSCRGKPKCYEEEQCVFLVAELKNDIESKSLVLKGCSNVSNATCQFLSGENK
TLGGVI FRKFECANVNSLTPTSAPTTSHNVGSKASLYLLALASLLLRGLLP

FIGURE 213

GGCCTCGGTTCAAACGACCCGGTGGGTCTACAGCGGAAGGGAGGGAGCGAAGGTAGGAGGCCA
 GGGCTTGCCCTCACTGGCCACCCCTCCCAACCCCAAGAGCCCAGCCCC**CAT**GTCCCCGCCGCCG
 GCGCGCTGCTGTGGGTCTGTGCTGAATCTGGGTCCCCGGCGCGCGGGGGCCCAAGGCCTG
 ACCCAGACTCCGACCGAAATGCAGCGGGTCAGTTTACGCTTTGGGGGCCCCATGCCCGCAG
 CTACCGGAGCACCGCCCGACTGGTCTTCCCCGGAAGACAAGGATAATCCTAGAGGACGAGA
 ATGATGCCATGGCCGACGCCGACCGCCTGGCTGGACCAGCGGCTGCCGAGCTCTTGGCCGCC
 ACGGTGTCCACCGCTTTAGCCGGTCGTCCGCCATTAACGAGGAGGATGGGTCTTCAGAAGA
 GGGGGTTGTGATTAATGCCGGAAGGATAGCACCAGCAGAGAGCTTCCCAGTGCAGACTCCCA
 ATACAGCGGGAGTTCCAGCACGAGGTTTATAGCCAATAGTCAGGAGCCTGAAATCAGGCTG
 ACTTCAAGCCTGCCGCGCTCCCCGGGAGGTCTACTGAGGACCTGCCAGGCTCGCAGGCCAC
 CCTGAGCCAGTGGTCCACACCTGGGTCTACCCGAGCCGCTGGCCGTACCCCTCACCACAG
 CCATGCCATCTCCTGAGGATCTGCGGCTGGTGTGATGCCCTGGGGCCCGTGGCACTGCCAC
 TGCAAGTCGGGCACCATGAGCCGGAGCCGCTCTGGGAAGCTGCACGCGCTTTCGGGGCGCT
 TCGAGTTGGGGCGCTGAGCCAGCTCCGCACGGAGCACAAGCCTTGCACTATCAACAATGTC
 CCTGCAACCGACTTCGGGAAGAGTGCCCCCTGGACACAAGTCTCTGTACTGACACCAACTGT
 GCCTCTCAGAGCACCACAGTACCAGGACCACCACTACCCCTTCCCCACCATCCACCTCAG
 AAGCAGTCCCAGCCTGCCACCCGCCAGCCCTGCCCAGCCCTGGCTTTTGGAAACGGGTCA
 GGATTGGCCTGGAGGATATTTGGAATAGCCTCTCTTCAGTGTTACAGAGATGCAACCAATA
 GACAGAAACCAGAGG**TAA**TGGCCACTTCATCCACATGAGGAGATGTCAGTATCTCAACCTCT
 CTTGCCCTTTCAATCCTAGCACCCACTAGATATTTTAGTACAGAAAAACAACTGGAAAA
 CACAA

FIGURE 214

MVFAAGALLWVLLNLGPRAAGAQGLTQTPTEMQRVSLRFGGPMTRSYSRSTARTGLPRKTRI
ILEDENDAMADADRLAGPAAELLAATVSTGFSRSSAINEEDGSSEEGVVINAGKDSTSREL
PSATPNTAGSSSTRFIANSQEPEIRLTSSLPRSPGRSTEDLPGSQATLSQWSTPGSTPSRWP
SPSPTAMPSPEDLRLVLMWPWGPWHCHCKSGTMSRSRSGKLHGLSGRLRVGALSQLRTEHKPC
TYQQCPCNRLREECPLDTSLCTDNCASQSTTSTRTTTTPFPTIHLRSSPSLPPASPCPALA
FWKRVRIGLEDIWNSLSSVFTEMQPIDRNQR

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FIGURE 215

CCGGGTCGAGCCACGCGTCGCGGGAGAAAGGATGCCGCGCTGGCGGCGGGTTGGTCTGCTAGCTGGGGCA
 GCGGCGCTGGCGAGCGGCTCCAGGGCGACCGTGAGCCGGTGTACCGCGACTGCGTACTGCAAGTGGGAAGCA
 GAATGCTCTGGGGCGCTCTGAATCACTCCGCTCCCGCCAGCCAACTACATGAGTCTAGCAGGCTGGACCT
 GTCCGGGACGACTGTAAAGTATGAGTGTATGTGGGTACCGCTGGGCTCTACCTCCAGGAAGTACAAAGTGCCCT
 CAGTTCATGGCAAGTGGCCCTCTCCCGGTTCTCGTTCTTTCAAGAGCGCGCATCGGCGCTGGCCTCGTTTCT
 CAATGGCCTGGCCAGCTGGTGATGCTCTGCCGTACCGCACCTTGGTCCAGAGCTCTCCCGCATGTACCA
 CCTGTGTGGCCTTCGCTGGGTGTCCCTCAATGATGGTTCTGGTCCACAGTCTTCCACACCGAGGACACTGAC
 CTCACAGAGAAATGGACTACTTCTGTGCTCCACTGTATCTTACACTCAATCTACCTGTGCTGCGTCAGGAC
 CGTGGGCTGCAGCACCGAGCTGTGGTCAGTGCCTTCGCGGCTCTCCTGCTGCTCATGCTGACCGTGCACGTCT
 CCTACCTGAGCCTCATCCGCTTCGACTATGGCTACAACCTGGTGGCCAACGTGGCTATTGGCCTGGTCAACGTG
 GTGTGGTGGCTGGCCTGGTGCCTGTGGAACACGCGCGGCTGCCTCACGTGGCAAGTGCCTGGTGGTGGTCTT
 GCTGCTGACGGGGCTGTCCCTGCTCGAGCTGCTTGACTTCCACCGCTCTTCTGGGTCTGGATGCCATGCCA
 TCTGGCAGATCAGCACCCTCCCTGTCCACGTCTCTTTTTCAGCTTTCTGGAAGATGACAGCCTGTACCTGCTG
 AAGGAATCAGAGGACAAGTTCAAGCTGGACTGAGACCTTGGAGCGAGTCTGCCCGAGTGGGGATCTGCCCC
 GCGCTGTGGCCTCCCTTCTCCCTCAACCTTGGAGTATTTCTCTTTTCAACTTCTTGAATCTGGACATGA
 AGGATGTGGGCCCAGAATCATGTGGCCAGCCACCCCTGTGGCCCTCACCAGCTTGGAGTCTGTTCTAGGG
 AAGCCTCCAGCATCTGGGACTCGAGAGTGGGCGAGCCCTTACCTCTGGAGCTGAAGTGGGGTGGAACTGA
 GTGTGTTCTTAGCTCTACCGGGAGGACAGCTGCCTGTTCTTCCCGCCAGCCTCTCCCCACATCCCACTG
 CTTGGCTGGGTCTGAAGCCTCTGTCTACCTGGGAGACGAGGACCAAGCCCTTAGGGATACAGGGGGTCCC
 TTTCTGTATACACCCCCACCTCTCCTCAGGACACCACTAGGTGGTGTGGTGTCTTCTTCTTGGCCAGCA
 GGTTCAGCGGATCTCCCATGGATCTTGGGGACCAAGCTGCTGGATTTGGGAAGGAGTTTCAACCTGACC
 GTTGCGCTCAGCTGAGTCTCCAGGAGCCTCACCATCTCCCTTTCAGGGCCAGGCTCCAGCAAGCCAGGCA
 AGGATCTGTGTCTGTCTGGTGTGAGAGCCTGCCACCGTGTGTGCGGAGTGTGGGCCAGGCTGAGTGCATAGG
 TGACAGGGCCCTGAGCATGGCCTGGGTCTGTGTGAGCTCAGGCCTAGGTGCGCATGTGAGACCGGTGTGT
 CGGGGAAGAGTGTGGCTTCAAAGTCTGTGTGTGACAGGGGGTGGGTGTGTAGCTGTGGTTAGGGGAAGCTGT
 TGCGCTGCTGTGGGCGATGAGATGAGTACTGCCGCTGAATGTGTCCACAGTTGAGAGGTTGGAGCAGGAT
 GAGGGAATCTGTCAACATCAATATCACTTGTGGAGCGCCAGCTGTGCCAAGACGCGCACCTGGGCGGACAGC
 CAGGAGCTCTCCATGGCCAGGCTGCCTGTGTGCATGTTCCCTGTCTGGTGCCCTTTGCCCGCTCTGTCAAAAC
 CTCACAGGGTCCCCACACAAGCTGCCCTCCAGAGCAGCCCTCGGAGGAGAGGAAAGAAATGGGATGGC
 TGGGGCTCTCTCCATCTCTCTTTCTCTTGCCTTCGATGGCTGGCCTTCCCCCTCAAAAACCTCCATCCCCCT
 GCTGCCAGCCCTTGGCATAGCCTGATTTGGGGAGGAGGAAGGGGCGATTTGAGGGAGAAGGGGAGAAAGCT
 TATGGCTGGGTCTGGTTTCTCCCTTCCAGAGGGTCTTACTGTTCAGGGTGGCCCCAGGGCAGGAGGGGCC
 ACATATGCTGTGCCCTGGTAAGGTGACCCCTGCCATTACAGCAGCCTGGCATGTTCTGCCCCACAG
 AATAGATGGAGGGAGCTCCAGAACTTCCATCCCAAAGGCGAGTCTCCGTGGTTGAAGCAGACTGGATTTTGT
 CTCGTCCCCTGACCCCTTGTCCCTTTGAGGGAGGGGAGCTATGCTAGGACTCCAACCTCAGGAACTCGGGT
 GCCTGCGCTAGCTCTTTTGATACTGAAAACCTTTAAGTGGGAGGTGGCAGCGATGTGCTTAATAAATCAA
 TTCCAAGCCTCAAAAAAAAAAAAAAAAAA

FIGURE 216

MAGLAARLVLLAGAAALASGSQGDREPVYRDCVLQCEEQNCSGGALNHFRSRQPIYMSLAGW
 TCRDDCKYECMWVTVGLYLQEGHKVPQFHGKWPFSSRFLFFQEPASAVASFLNGLASLVMLCR
 YRTFVPASSPMYHTCVAFAWVSLNAWFSTVFHTRDLDLTKMDYFCASTVILHSIYLCCVR
 TVGLQHFAVVSAFRALLLMLTVHVSYSLSLIRFDYGYNLVANVAIGLVNVVWWLAWCLWNQR
 RLPHVRKCVVVLLQLGLSLELLDFPPLFWVLDAAHAIWHISTIPVHVLFSSFLEDDSLYLL
 KESEDKFKLD

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domains:

amino acids 105-123, 138-156, 169-185, 193-209, 221-240, 256-272

N-glycosylation site.

amino acids 40-44

N-myristoylation site.

amino acids 43-49

CUB domain proteins profile.

amino acids 285-302

Amiloride-sensitive sodium channels proteins.

amino acids 162-186

FIGURE 217

[illegible]

FIGURE 218

MAPQSLPSSRMAPLGMLLGLLMAACFTFCLSHQNLKEFALTNPESSTKETERKETKAEEL
 DAEVLEVFHPTHEWQALQPGQAVPAGSHVRLNLQTGEREAKLQYEDKFRNNLKGKRLDINTN
 TYTSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVVIETDMQIMV
 RLINKFNSSSSSLEEKIAALFDLEYVYVHQMDNAQDLLSFGGLQVVINGLNSTEPLVKEYAAF
 VLGAAFSSNPKVQVEAIEGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYAQRQFLKL
 GGLQVLRITLVQEKGTEVLAVRVVTLTYDLVTEKMFEEEEAELTQEMSPEKLQQYRQVHLLPG
 LWEQGWCEITAHLLALPEHDAREKVLQTLGVLLTTCRDYRQDPQLGRTLASLQAEYQVLAS
 LELQDGEDEGYFQELLGSVNSLLKELR

Important features:

Signal peptide:

amino acids 1-29

Hypothetical YJL126w/YLR351c/yhcX family protein.

amino acids 364-373

N-glycosylation site.

amino acids 193-197, 236-240

N-myristoylation site.

amino acids 15-21, 19-25, 234-240, 251-257, 402-408, 451-457

Homologous region SLS1 protein.

amino acids 68-340

FIGURE 219

TTCGGCTTCGCTAGAGGAAGTGGCGCGGACCTTCATTGGGGTTTCGGTTCCCCCCTTCCC
 CTTCCCCGGGGTCTGGGGGTGACATTGCACCGCGCCCCCTCGTGGGGTCGGGTTGCCACCCCA
 CGCGGGACTCCCCAGCTGGCGCGCCCCCTCCCATTTGCCTGTCTCTGGTCAGGCCCCACCCCC
 TTTCCACCTGACCAGCCATGGGGGGCTGCGGTGTTTTTCGGCTGCACTTTCTGTCGCGTTCGGC
 CCGGCCTTCGCGCTTTTCTTGATCACTGTGGCTGGGGACCCGCTTCGCGTTATCATCTCGGT
 CGCAGGGGCATTTTTCTGGCTGGTCTCCCTGTCTCTGGCCTCTGTGGTCTGGTTTCATCTTGG
 TCCATGTGACCGACCGGTGAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTTGGTGCTGCT
 GTCTCTGTCTCTTACAGGAGGTGTTCCGCTTTCCTACTACAAGCTGCTTAAGAAGGCAGA
 TGAAGGGTTAGCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCGAGATGGCCT
 ATGTTTTCTGGTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTATCAATATTTGGCT
 GATGCACCTTGGGCCAGGTGTGGTTGGGATCCATGGAGACTCACCCATTACTTCTGACTTC
 AGCCTTCTGCAGCAGCCATTATCCTGCTCCATACCTTTTGGGGAGTTGTGTTCTTTGATG
 CCTGTGAGAGGAGACGGTACTGGGCTTTGGGCTGGTGGTTGGGAGTCACTACTGACATCG
 GGACTGACATTCCTGAACCCCTGGTATGAGGCCAGCCTGCTGCCCATCTATGCAGTCACTGT
 TTCCATGGGGCTCTGGGCTTTTCATCACAGCTGGAGGGTCCCTCCGAAGTATTCAGCGCAGCC
 TCTTGTGTAAGGACTGACTACCTGGACTGATCGCCTGCAGATCCACCTGCCTGTCCACTG
 CCCATGACTGAGCCAGCCCCAGCCCGGGTCCATTGCCACATTCTCTGTCTCCTTCTCGTC
 GGTCTACCCCACTACCTCCAGGTTTTGCTTTGTCCCTTTTGTGACCGTTAGTCTCTAAGCTT
 TACCAGGAGCAGCTGGGTTACGCCAGTCAGTGACTGGTGGGTTTGAATCTGCACCTATCCC
 CACCACCTGGGGACCCCTTGTGTGTCCAGGACTCCCCCTGTGTGCTGCTGTCTGTCTCAC
 CCTGCCAAGACTCACCTCCCTTCCCTCTGCAGGCCGACGGCAGGAGGACAGTCGGGTGAT
 GGTGTATTTCTGCCCTGCGCATCCCACCCGAGGACTGAGGGAACCTAGGGGGGACCCCTGGGC
 CTGGGGTGCCCTCCTGATGTCTCGCCCTGTATTTCTCCATCTCCAGTTCTGGACAGTGACG
 GTTGCCAAGAAAAGGGACCTAGTTTAGCCATTGCCCTGGAGATGAAATTAATGGAGGCTCAA
 GGATAGATGAGCTCTGAGTTTCTCAGTACTCCCTCAAGACTGGACATCTTGGTCTTTTTCTC
 AGGCCCTGAGGGGGAACCATTTTTGGTGTGATAAAATCCCTAAACTGCCTTTTTTCTTTTTT
 GAGGTGGGGGGAGGGAGGAGGTATATTTGGAACCTCTTCAACCTCCTTGGGCTATATTTCTC
 TCCTCGAGTTGCTCCTCATGGCTGGGCTCATTTCGGTCCCTTCTCTCTTGGTCCACGACCTT
 GGGGSAAGGAAGGAAGTGCATGTTTGGGAACCTGGCATTACTGGAACATAATGGTTTTAACCT
 CCTTAACCACCAGCATCCCTCCTCTCCCCAAGGTGAAGTGGAGGGTGTCTGTGGTGAGCTGGC
 CACTCCAGAGCTGCAGTGCCACTGGAGGAGTGCAGACTACCATGACATCGTAGGGAAGGAGGG
 GAGATTTTTTTGTAGTTTTTAATTGGGGTGTGGGAGGGGCGGGGAGGTTTTCTATAAAGTGT
 ATCATTTTTCTGCTGAGGGTGGAGTGCCCATCCTTTTAATCAAGGTGATTGTGATTTTGACT
 AATAAAAAAGAAATTTGTAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA
 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA

FIGURE 220

MGAAVFFGCTFVAFGPAFALFLITVAGDPLRVIIIVAGAFFWLVSLLLASVVWFILVHVTDR
SDARLQYGLLIFGAAVSVLLQEVFRFAYYKLLKKADEGLASLSEDRSPISIRQMAYVSGLS
FGIISGVFVSVINILADALGPGVVGIIHGDSPIYFLTSAFLTAAILLHTFWGVVFFDACERRR
YWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRSIQRSLCKD

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AAGCTGGTTTAAGGAAGCAGAGGAGGGTTAGATTCTGTGAGTGAGGACGGAAGATCAACCCA
 TTTCCATTCGCCAGATGGCCTATGTTTCTGGTCTCTCCCTCGGNATCATCAGTGGTGTNT
 TNTCTGTTATCAATATTTGGCTGATGCANTTGGGCCAGGTGTGGTTGGGATCCATGAGAGC
 TCACCCATTANTTCTGAN TTCAGCCTTTNTGACAGCAGCCATTATCCTGCTC

FIGURE 222

GACCGACCGTTCAGATGCCCGGTTCCAGTACGGCTTCTGATTTTTGGTGCTGCTGTNTCTG
TCCTTCTACAGGAGGTGTTCCGCTTTGCCTANTACAAGCTGCTTAAGAAGGCAGATGAGGGG
TTAGCATNGCTGAGTGAGGACGGAAGATCACCCATTTCCATCCGCCAGATGGCCTATGTTTN
TGGTNTTTCCTTCGGTATCATCAGTGGTGTNTCTGTTATCAATATTTGGNTGATGCAN
TTGGGCCAGGTGTGGTTGGGATCCATGGAGANTCACCTATTAAATTCCTGAATTCAGCCTTT
NTGACAGCAGCCATTATCCTGNTCCATACCTTTGGGGAGTTGTGTTTTTGATGCCTGTGA
GAGGAG

FIGURE 223

NGTTGGAGAAGTGGCGCGGACNTTCATTTGGGGTTTCGGTTTCCCCCTTCCCTTTCCCCG
GGTCTGGGGTGACATTGCACGGGCCCCCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCC
CCAGNTGGNGCGCCCTTCCCATTTGCCTGTCCTGGTCAGGCCCCACCCCCCTTCCACNTG
ACCAGCCATGGGGGCTGCGGTGTTTTTCGGCTGCACCTTTCGTCGCGTTTCGGCCCGCCTTCG
CGCTTTTCTTGATCACTGTGGCTGGGGACCGCTTCGCGTTATCATCCTGGTCGAGGGGCA
TTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTTGGTCCATGTGAC
CGACCGGTCAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTTGGTGCTGCTGTCTGTGCC
TTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGATAGGGGGTTA
GCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTGG
TCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTGGCTGATGCACTTG
GGCCAGGTGTGGTTGGGATCCATGGAGACTCACCC

FIGURE 224

GTAAAAGAAAGTGGCCGGACCTTCATTGGGGTTTCGGTTCCCCCTTTCCCNNTTCCCCGGGG
TCTGGGGGTGACATTGCACCGCGCCNCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCCC
CAGNTGGCGCGCCCCCTCCCATTTGCCTGTCTGGTCAGGCCCCACCCCCCTTCCACCTGA
CCAGCCATGGGGGCTGCGGTGTTTTTCGGGCTGCACCTTCGTGCGGTTTCGGGCCCGGCCTTC
GCGCTTTTCTTGATCACTGTGGCTGGGGACCCGCTTCGCGTTATCATCCTGGTCGCAGGGGC
ATTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTTGGTCCATGTGA
CCGACCGGTCAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTTGGTGCTGTCTCTGTC
CTTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTT
AGCATCGCTGAGTGAGGACGGAAGATCACCATCTCCATCCGCCAGATGGCCTATGTTTCTG
GTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTGGCTGATGCACTT
GGGCCAGGTGTGGTTGGGATCCATGGAGAC

FIGURE 225

GCCCCAGGGAGCAGTGGGTGGTTATAACTCAGGCCCCGTGCCCAGAGCCCAGGAGGAGGCAG
 TGGCCAGGAAGGCACAGGCTGAGAAGTCTGCGGCTGAGCTGGGAGCAAATCCCCACCCCC
 TACCTGGGGACAGGGCAAGTGAGACCTGGTGAGGTGGCTCAGCAGGCAGGGAAGGAGAGG
 TGTCTGTGCGTCTTCACCCACATCTTTCTCTGTCCCTCCTTGCCCTGTCTGGAGGCTGCT
 AGACTCCTATCTTCTGAATTCATAGTGCCCTGGGTCTCAGCGCAGTGCCGATGGTGGCCCGT
 CCTTGTGGTTCCTCTCTACCTGGGGAATAAGGTGCAGCGGCCATGGGCTACAGCAAGACCCC
 CCTGGATGTGGGTGCTCTGTGCTCTGATCACAGCCTTGCTTCTGGGGGTCACAGAGCATGTT
 CTCGCCAACATGATGTTTCTGTGACCACCCCTCTAACACCGTGCCCTCTGGGAGCAACCA
 GGACCTGGGAGCTGGGGCCGGGAAGACGCCCGGTGCGATGACAGCAGCAGCCGCATCATCA
 ATGGATCCGACTGCGATATGCACACCCAGCCGTGGCAGGCCGCGCTGTTGCTAAGGCCAAC
 CAGCTCTACTGCGGGCGGTGTTGGTGCATCCACAGTGGCTGCTCACGGCCGCCCACTGCAG
 GAAGAAAGTTTTCAGAGTCCGTCTCGGCCACTACTCCCTGTACCAGTTTATGAATCTGGGC
 AGCAGATGTTCCAGGGGTCAAATCCATCCCCACCCCTGGCTACTCCCACCCTGGCCACTCT
 AACGACCTCATGCTCATAAACTGAACAGAAGAATTCGTCCCACTAAAGATGTCAGACCCAT
 CAACGTCTCCTCTCATTGTCCCTCTGCTGGGACAAAGTGCTTGGTGTCTGGCTGGGGACAA
 CCAAGAGCCCCAAGTGCACTTCCCTAAGGTCTCCAGTGCTTGAATATCAGCGTGCTAAGT
 CAGAAAAGGTGCGAGGATGCTTACCCGAGACAGATAGATGACACCATGTTCTGCGCCGGTGA
 CAAAGCAGGTAGAGACTCCTGCCAGGGTGATTCTGGGGGGCCTGTGGTCTGCAATGGCTCCC
 TGCAGGGACTCGTGTCTGGGGAGATTACCCTTGTCGCCGGCCCAACAGACCGGGTGCTTAC
 ACGAACCTCTGCAAGTTCACCAAGTGGATCCAGGAAACCATCCAGGCCAACTCCTTGAGTCAT
 CCCAGGACTCAGCACACCGGCATCCCCACCTGCTGCAGGGCAGCCCTGACATCCTTTCAG
 ACCCTCATTCCTTCCCAGAGATGTTGAGAATGTTTACTCTCTCCAGCCCCGACCCCATGTCT
 CCTGGACTCAGGGTCTGCTTCCCCACATTGGGCTGACCGTGTCTCTAGTTGAACCCCTGG
 GAACAATTTCCAAAAGTGTCCAGGGCGGGGTGCGTCTCAATCTCCCTGGGGCACTTTCAT
 CCTCAAGCTCAGGGCCCATCCCTTCTCTGCAGCTCTGACCCAAATTTAGTCCAGAAATAAA
 CTGAGAAAGTGAAAAAAA

FIGURE 226

MATARPPWMWVLCALITALLGVTEHVLANNNDVSCDHPSNTVPSGSNQDLGAGAGEDARSDD
SSSRIINGSDCDMHTQPWQAALLLRPNQLYCGAVLVHPQWLLTAAHCRKKVFRVRLGHYSLS
PVYESGQQMFQGVKSIHPHGYSHPGHSNDLMLIKLNRRIPTKDVRPINVSSHCPISAGTKCL
VSGWGTTKSPQVHFVKVLQCLNISVLSQKRCEADAYPRQIDDTMFCAGDKAGRDSCQGDSSGP
VVCNGSLQGLVSWGDYPCARPNRPGVYTNLCKFTKWIQETIQANS

1000
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[illegible]

FIGURE 228

MVNDRWKTMGGAAQLEDPRDKPQRPSCGYVLCTVLLALAVLLAVAVTGAVLFLNHAHAPGT
APPPVVSTGAASANSALVTERADSSHLSILIDPRCPDLTDSFARLESAQASVLQALTEHQA
QPRLVGDQEQLLDTLADQLPRLLARASELQTECMGLRKHGHTLGQGLSALQSEQGRLIQLL
SESQGHMAHLVNSVSDILDALQRDRGLGRPRNKADLQRAPARGTRPRGCATGSRPRDCLDVL
LSGQQDDGVYSVFPPTHYPAGFQVYCDMRTDGGGWTVFQRREDGSVNFFRGWDAYRDGFGRLT
GEHWLGLKRIHALTTQAAYELHVDLEDFENGTAAYARYGSFGVGLFSVDPEEDGYPLTVADYS
GTAGDSLKKHSGMRFTTKDRSDHSENNCAAFYRGAWWYRNCHTSNLNGQYLARGAHASYADG
VEWSSWTGWQYSLKFSEMKIRPVREDR

FIGURE 229

GCAGTCAGAGACTTCCCCTGCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTTAGTGCCT
 TGCTTCTGAAGTACAGTACAGTACCCGGCGGCCAGGGCAATCCGACCACATTTACTCT
 CACCGCTGTAGGAATCCAG**ATG**CAGGCCAAGTACAGCAGCACGAGGGACATGCTGGATGATG
 ATGGGGACACCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACCTCGGCATCCAGAGCCC
 CGGCGCACAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCCTGCTGAC
 TTTGTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTACTACC
 AGCTCTCCAATACTGGTCAAGACACCATTTCTCAAATGGAAGAAAGATTAGGAAATACGTCC
 CAAGAGTTGCAATCTCTTCAAGTCCAGAATATAAAGCTTGCAAGGAAGTCTGCAGCATGTGGC
 TGA AAAA ACTCTGTGCTGAGCTGTATAACAAAGCTGGAGCACACAGGTGCAGCCCTTGACAG
 AACAAATGGAATGGCATGGAGACAATTGCTACCAGTTCATAAAGACAGCAAAAGTTGGGAG
 GACTGTAAATATTTCTGCCTTAGTGAAAACCTACCATGCTGAAGATAAACAACAAGAAGA
 CCTGGAATTTGCCGCTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGACAGGGCTTT
 TGGCCCTTGACAGTGGCAAGGCCTGGCTGTGGATGGATGGAACCCCTTTCACCTCTGAACTG
 TTCATATTTATAATAGATGTCACCAGCCCAGAAGCAGAGACTGTGTGGCCATCCTCAATGG
 GATGATCTTCTCAAAGGACTGCAAAGAATTGAAGCGTTGTGTCTGTGAGAGAAGGGCAGGAA
 TGGTGAAGCCAGAGAGCCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGAC**TGA**TTTCGCC
 CTCTGCAACTACAAATAGCAGAGTGAGCCAGGCGGTGCCAAAGCAAGGGCTAGTTGAGACAT
 TGGGAAATGGAACATAATCAGGAAAGACTATCTCTCTGACTAGTACAAAATGGGTTCTCGTG
 TTCTCTGTTCAGGATCACCAGCATTTCTGAGCTTGGGTTTATGCACGTATTTAACAGTCACA
 AGAAGCTTATTTACATGCCACCAACCAACCTCAGAAACCCATAATGTCATCTGCCTTCTTG
 GCTTAGAGATAACTTTTAGCTCTCTTTCTTCTCAATGTCTAATATCACCTCCCTGTTTTCAT
 GTCTTCTTTACACTTGGTGAATAAGAAACTTTTTGAAGTAGAGGAAATACATTGAGGTAAC
 ATCCTTTTCTCTGACAGTCAAGTAGTCCATCAGAAATTGGCAGTCACTTCCCAGATTGTACC
 AGCAAATACACAAGGAATTTCTTTTGTGTTTTCAGTTTCACTAGTCCCTTCCCAATCCAT
 CAGTAAGACCCCATCTGCCTTGTCCATGCCGTTTCCCAACAGGGATGTCACTTGATATGAG
 AATCTCAAATCTCAATGCCTTATAAGCATTCTTCTGTGTCCATTAAAGACTCTGATAATTG
 TCTCCCTCCATAGGAATTTCTCCAGGAAAGAAATATATCCCATCTCCGTTTCATATCAG
 AACTACCGTCCCCGATATTTCCCTTCAGAGAGATTAAAGACCAGAAAAAAGTGAGCCTTTCA
 TCTGCACCTGTAATAGTTTCAGTTCCTATTTTCTTCCATTGACCCATATTTATACCTTTCA
 GTACTGAAGATTTAATAATAATAAATGTAATACTGTGAAAAA

FIGURE 230

MQAKYSSTRDMLDDDDGDTTMSLHSQASATTRHPEPRRTEHRAPSSTWRPVALTLLTLCVLVLL
IGLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCRE
LYNKAGAHRCSPCTEQWKWHGDNQYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFAAS
QSYSEFFYSYWTGLLRPDSGKAWLWMDGTPFTSELFHIIIDVTSPRSRDCVAILNGMIFSKD
CKELKRCVCERRAGMVKPESLHVPPETLGEGD

FIGURE 231

AATTTTCACCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGNTGG
ATGATGATGGGACACCACCATGAGCCTGCATTNTCAAGCTTTTGCCACAATTCGGCATCCAG
AGCCCCGGCGCACAGAGCACAGGNTCCTTTTCAACGTGGCGACCAAGTGGCCCTGACCCCTG
CTGACTTGTGCTTGGTGTCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTA
CTACCAGCTCTCCAATACTGGTCAAGACACCATTCTCAAATGGAAGAAAAGATTAGGAAATA
CGTCCCAGAGTTGCAATTNTTCAAGTCCAGAATATAAAGCTTGCAAGGAAGNTGCAGCAT
GTGGCTGAAAACTCTGTCGTGAGCTGTATAACAAAGCTGGAGGAACCTTTGAAGGAGGGCAA
AGTNTCCTCATNTACTATACACACCACTTCCC



FIGURE 232

CGCAGAGCGCAAGAACCTTCGCGCAGCCAGAGCAGCTGCTGGAGGGGAATCGAGGCGCGGCTC
CGGGAGCTTCGGCTTCGGGCGCGCTGGCTCTGCTCTGCGGCGGAGGAGCGGGCGCGCCGCGGGG
CCCGAGCCCTCCGGATCCGCCCTCCCGGCTCCGCGCCCTCGGAGACCTCTCTGGCTGCT
TCGGGGGTTTCGCCGGGGCGGGGACCCGCGGTCCGGCGGCC**ATG**CGGGGCATTCGCTGCTGCT
TCGGTGTCTGCGGCGCGCAGGGCGCTGGCCGTGGGCACTTCCTGGGCTACCTTGAGCTCT
GCTCAGCTTCACCTGGGTGGAGGAGCGCTGCGGCCAGGCCGCCCACTTGAGACTCTG
AGTCGCGCGCGGGGAACCAACCAACGCGCGCGCCCAACTCGGTGCAGCGCCGAGCG
GAGCGCGAGAAGCCCGGGGCGCGGGAAGGCGCGGGGAGAATTGGGAGCGCGCGTCTTGCC
CTACCACTCTGCAGACCGCGCGCAGGCCGCCAAAGGCGCTCAGGACCCGCTACATCAGC
CGGAGCTGGGCATCAGCAGAGGCTGCTGTGGCGGTGCTGACCTTCAGAACCGCTGCC
ACGCTGGGCTGGCGCTGAACCGCACGCTGGGGCACCGGCTGGAGCTGTGGTGTTCCTGAC
GGCGCAGCGGGCGCGCGGCCCCACCTGCGATGCGATGGCATGTTGTCAGCTGGCGAGGAGC
CGATTGGACACCTGCACTGCGCTGCGCGACCTGCTGGAGACGACCGCGCAGCTTACG
TGTTTCTTCTGTGCTCTGACACCACCTACACCAGGCGCAGCGCTGGCAGCGCTTAAGTGG
CCACCTCAGCTTGGCTTCGCGCGCCACCTGTACCTGGGCGCGGCCCAGGACTTCATCGGG
GAGAGCCACCCCGCGCGCTACTGCGCAGGAGGCTTTGGGTGCTGCTGTGCGCGATGCTG
CTGCACAACTCGCCGCCACCTGGAAGCTGCGCAACGACATCGTACTGCGGCCCTGA
CGAGTGGCTGGTTCGCTGCATTCTCATGTCGCCACGGGTGGGCTGCATGTTGACCCAGG
GGGTGACCTATGAGCAATTCGAGCTGAGCCCTGGGAGAGCTGACGAGGGGGGACCCCTAG
TTCCGAAGTGCCTGACGCCACCCCTGTGCTGACCTGTGCATATGTACAGCTGCACAA
AGCTTTCCGCCAGCTGAACCTGGAACGCACTACAGGAGATCCAGAGATTACAGTGGAGA
TCCAGAATACCAGCCATCTGGCCGTTGATGGGAGCGGGCAGCTGCTTGGCCCTTGGGTATT
CCAGCACCATCCCGCGCGCTCCCGCTTTGAGGTGCTGCGCTGGGACATCTCACGAGCA
GCAGCTTTTCTCTGCGCGATGGTCAACCCGCTGCCACATGCTGGCTGGGGCTGACCGGGT
ATGTGGCGCAGTGTTCTGGGACAGCTCTAGAGGAGCTGAACCCGCGCTACCAACCGGCCTT
CGGCTCCAGAAGCAGCAGCTGGTGATGTGCTACGACAGCTTTGATCGCGCCGGGTATGGA
ATACAGCTGGACTTCAGCTGGAGCAGCTGACCCCAAGGAGGCGCGGCCCTCACTC
CCGAGTGCAGCTGCTCGCGCCGCTGAGCGCGCTGGAGATCTTGCTTGTGCCCTATGTCACT
GAGGCTCTACGCTCTACTGTGCTGTGCTCTAGCTGCGGCTGAGCTGACCTGGCCCTTGG
CTTCTTGGAGGCTTTTGGCACTGACAGCTGGAGCTGGTGATGCTGCGGACCGCTGACC
TGCTGCTACTGTATGAGCGCGCGCAGGCCACGCGGTGGCCATCGAGATGCTTCGCACTT
GTCAAGGCCCACTGGCAGAGCTGGAGCGCGCTTTCCCGGTGCGCGGTGCCATGGCTCAG
TGTGCAGACAGCGCGCACTCACTACCTCGCGCTCATGATCTACTCTCAAGAAGACACCGC
TGGCACACTGTTCTGCTGTCGCGGGCGAGACAGCTGTCTCAGCGCTGACTTCTTCAACCG
TGCGCATGATGCACTCTCTCGGCTGGCAGGCTTCTTCCATGATTTCAAGCTTCCA
CCGAGTTGTGGCCCAACCAAGGGCTTGGGCCCAAGAGCTGGGCGGTGACATGGCCGCT
TTGATCGCAGGCAACGAGCGAGGCTGCTTCAACAATCCGATACGTGGCAGCCGTGGG
CGCTTGGCGGCGAGCTCAGAACAAGAGAGGAGCTGCTGGAGAGCTTGAATGTGTACAGCT
GTTCTCCACTTCTCCAGTCTGCATGTGCTTGGGGCGGTGGAGCGCGGCTGCTGCAGCGCT
ACCGGCGCCAGAGCTGCAGCGCGAGGCTCAGTAGGACCTGTACCCAGTGGCTGCCACGAG
GTGCTTGAAGGCTCTCGCTCCGGAACCCAGCTGCCATCTGACTACTTTGAACAGCAGAGG
CAACAGCACT**TG**ACCCACCTCTGCCCGTGGCGCGTGTCATGGCCACCCACCCCACT
CTCCGCCAAAACAGAGCAACCTGCGAGCTCTGCTGGCAGGGCTGGCCCTGACAGACCCC
AAGCTGGCCCACTGGTCCCCTCTGAGCTCTGTGGTCCCTGGGCTCTGAGCAAGCACTGG
GGAGTGGCCCAAGAGCCACCCACTTCTCATCCCAACCCAGTTTCCTGCGCCCTGACGCT
GCTGATTCGGGCTGTGGCTCCCACTATTATGATGACATGCTGCTGACGCCAGCCCTG
CTTGGGCGCTGGGGCTGGGCTGTAGAAGATGTTTGGGAAGGAGGAGCTGAGGAGGG
GCACTCCAACATCTCCCTTTTGACCCCTGCCGAAGCTCCCTGCCTTTAATAAATGGCCA
AGTGTGGAAGAA

FIGURE 233

MRASLLLSVLRPAGPVAVGISLGF T L S L L S V T W V E E P C G F G P P Q P G D S E L P P R G N T N A A R R P
NSVQPGAEREKPGAGEGAGENWEPRVLPYHPAQPGQAACKAVRTRYISTELGIRQRLLVAVL
TSQTTLPTLGAVNRTLGHRLERVVFLTGARGRRAPPGMAVVTLGEERPIGHLHLALRHLE
QHGD D F D W F F L V P D T T Y T E A H G L A R L T G H L S L A S A A H Y L G R P Q D F I G G E P T P G R Y C H G G F G
V L L S R M L L Q Q L R P H L E G C R N D I V S A R P D E W L G R C I L D A T G V G C T G D H E G V H Y S H L E L S P G E P
V Q E G D P H F R S A L T A H P V R D P V H M Y Q L H K A F A R A E L E R T Y Q E I Q E L Q W E I Q N T S H L A V D G D R A
A A W P V G I P A P S R P A S R F E V L R W D Y F T E Q H A F S C A D G S P R C P L R G A D R A D V A D V L G T A L E E L N
R R Y H P A L R L Q K Q Q L V N G Y R R F D P A R G M E Y T L D L Q L E A L T P Q G G R R P L T R R V Q L L R P L S R V E I
L P V P Y V T E A S R L T V L L P L A A A E R D L A P G F L E A F A T A A L E P G D A A A A L T L L L L Y E P R Q A Q R V A
H A D V F A P V K A H V A E L E R R F P G A R V P W L S V Q T A A P S P L R L M D L L S K K H P L D T L F L L A G P D T V L
T P D F L N R C R M H A I S G W Q A F F P M H F Q A F H P G V A P P Q G P G P P E L G R D T G R F D R Q A A S E A C F Y N S
D Y V A A R G R L A A A S E Q E E L L E S L D V Y E L F L H F S S L H V L R A V E P A L L Q R Y R A Q T C S A R L S E D L
Y H R C L Q S V L E G L S R T Q L A M L L F E Q E Q G N S T

FIGURE 234

GCTCTGGCGGCCCCGGCGATTGGTCACCGCCCGCTAGGGGACAGCCCTGGCCTCCTCTGAT
 TGGCAAGCGCTGGCCACCTCCCCACACCCCTTGCGAAGCGTCCCTAGTGGAGAAAAGGAGT
 AGCTATTAGCCAATTCGGCAGGGCCCGCTTTTAGAAGCTTGATTTCCTTTGAAGATGAAAG
 ACTAGCGGAAGCTCTGCCTCTTTCCCCAGTGGGCGAGGGAACTCGGGGCGATTGGCTGGGAA
 CTGTATCCACCCAAATGTACCGATTCTTCCTATGCAGGAAATGAGCAGACCCATCAATAA
 GAAATTTCTCAGCCTGGCCGAAAAATGGTTGGCCCCACGAAGCCACGACAACCTGGAGGCAAAG
 AGGGTTGCTCAACGCCCGCCTCATTGGA AAAACCAAATCAGATCTGGGACCTATATAGCGTG
 GCGGAGGCGGGGCGATGATTGTCGCGCTCGCACCCACTGCAGCTGCGCACAGTCGCATTTCT
 TTCCCCGCCCTGAGACCCTGCAGCACCATCTGTC**ATG**GCGGCTGGGCTGTTTGGTTTGAGC
 GCTCGCCGTCTTTTGGCGGCAGCGGCGACGCGAGGGCTCCCGGCCCGCCGCTCCGCTGGGA
 ATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCTGTGGCGGAAAGCGGCCCCCAGAAC
 CGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGACGAAACTTGATGAGAAGAACCCA
 GACTCCCATGGTTATGACAAGGACCCCGTTTGGACGCTCTGGAACATGCGACTTGCTTCTT
 CTTTGGCGTCTCCATCATCCTGGTCTTGGCAGCACCTTTGTGGCTATCTGCCTGACTACA
 GGATGAAAGAGTGGTCCCGCCGCGAAGCTGAGAGGCTTGTGAAATACCGAGAGGCCAATGCG
 CTTCCCATCATGGAATCCAACCTGCTTCGACCCAGCAAGATCCAGCTGCCAGAGGATGAG**TC**
ACCAGTTGCTAAGTGGGGCTCAAGAAGCACCGCCTTCCCCACCCCTGCCTGCCATTCTGAC
 CTCTTCTCAGAGCACCTAATTAAAGGGGCTGAAAGTCTGAA

GGCGGCTGGGCTGTTTGGTTTGAGCGCTCGCCGTCTTTTGGCGGCAGCGGCACGCGAGGGC
TCCGGGCGCGCCGCGTCCGCTGGGAATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCT
GTGGCGGGAAGCGGCCCCAGAACGCACACACCGTGGCAAGAGACCAGAACCAGAGA
CGAAAACCTGTATGAGAAGAACCCAGACTCCCATGTTATGACAAGACCCCGTTTGGACG
TCTGGAACATGCGACTTGTCTTCTTCTTTGGCGTCTCCATCATCCTGGTCCTTGGCAGCAC
TTTGTGGCCTATCTGCCTGACTACAGGATGAAAGAGTGGTCCGCGCGGAAGCTGAGAGGCT
TGTGAAATACCGAGAGGCCAATGGCCTTCCCATCATGGAATCCAAC TGCTTCAGCCCAGCA
AGATCCAG

FIGURE 237

GCGGCGGCT**ATG**CCGCTTGCTCTGCTCGTCTGTTGCTCCTGGGGCCCGGCGGCTGGTGCCT
 TGCAGAACCCCAACGCGACAGCCTGCGGGAGGAACCTTGTCATCACCCCGTGCTTCCGGGG
 ACGTAGCCGCCACATTCCAGTTCGCGACGCGCTGGGATTTCGAGCTTCAGCGGGAGGAGTG
 TCCCATTTACAGGCTCTTTCCCAAAGCCCTGGGGCAGCTGATCTCCAAGTATTTCTACGGGA
 GCTGCACCTGTCTATCACACAAGGCTTTTGGAGGACCCGATACTGGGGGCCACCCCTTCTGCTC
 AGGCCCATCAGGTGCAGAGCTGTGGGTCTGGTTCCAAGACACTGTCACTGATGTGGATAAA
 TCTTGGAAAGGAGCTCAGTAATGTCTCTCAGGGATCTTCTGCGCCTCTCTCAACTTCATCGA
 CTCACCAACACAGTCACTCCCACTGCCTCCTTCAAACCCCTGGGTCTGGCCAATGACACTG
 ACCACTACTTTCTGCGCTATGCTGTGCTGCCGCGGGAGGTGGTCTGCACCGAAAACCTCACC
 CCCTGGAAGAAGCTCTTGCCCTGTAGTTCCAAGGCAGGCCCTCTCTGTGCTGCTGAAGGCAGA
 TCGCTTGTTCACACACAGCTACCACTCCCAAGGCAGTGATATCCGCGCTGTTTGCGAGAAATG
 CACGCTGTACTAGCATCTCTCTGGGAGCTGAGGCAGACCTGTCAGTTGTATTTGATGCCTTC
 ATCACGGGGCAGGGAAAGAAAGACTGGTCCCTCTTCCGGATGTTCTCCCGAACCCCTCACGGA
 GCCTGCCCCCTGGCTTCAGAGAGCCGAGTCTATGTGGACATCACCACTACAAACAGGACAA
 ACGAGACATTAGAGGTGACCCACCCCGACCACTACATATCAGGACGTCATCCTAGGCATC
 CGGAAGACCTATGCCATCTATGACTTGCTTGACACCGCCATGATCAACAACCTCTCGAAACCT
 CAACATCCAGCTCAAGTGAAGAGACCCCCAGAGAATGAGGCCCCCCCAGTGCCCTTCTCTGC
 ATGCCAGCGGTACGTGAGTGGCTATGGGCTGCAGAAGGGGGAGCTGAGCACACTGCTGTAC
 AACACCCACCCATACCGGGCCTTCCCGGTGCTGCTGCTGGACACCGTACCTGGTATCTGCG
 GCTGTATGTGCACACCCTCACCATCACCTCCAAGGGCAAGGAGAACAAACCAAGTTACATCC
 ACTACCAGCCTGCCAGGACCGGCTGCAACCCACCTCCTGGAGATGCTGATTACAGTGCCTG
 GCCAACCTCAGTCACCAAGGTTTCCATCCAGTTTGAGCGGGCGCTGCTGAAGTGGACCGAGTA
 CACGCCAGATCCTAACCATGGCTTCTATGTACGCCCATCTGTCCTCAGCGCCCTTGTCGCCA
 GCATGGTAGCAGCCAAGCCAGTGGACTGGGAAGAGAGTCCCTCTTCAACAGCCTGTTCCTCA
 GTCTCTGATGGCTCTAACTACTTTGTGCGGCTCTACACGGAGCCGCTGCTGGTGAACCTGCC
 GACACCGGACTTCAGCATGCCCTACAACTGATCTGCCTCAGGTGCACTGTGGTGGCGGTGT
 GCTACGGCTCCTTCTCAATATCTCTCACCCGAACCTTCCACATCGAGGAGCCCCGCACAGGT
 GGCTGGCCAAAGCGCTGGCCAACCTTATCCGGCGCGCCCGAGGTGTCCCCCACTC**TG**AAT
 CTTGCCCTTTCCAGCAGCTGCAGCTGCCGTTTCTCTCTGGGAGGGGGAGCCCAAGGGCTGTT
 TCTGCCACTTGCTCTCCTCAGAGTTGGCTTTTGAACCAAAGTGCCCTGGACCAAGGTGAGGGC
 CTACAGCTGTGTTGTCCAGTACAGGACCCAGGACCAATGTGGCATTGAATTTGAATTA
 CTAGAAATTCATTTCCTCACCTGTAGTGGCCACCTCTATATTGAGGTGCTCAATAAGCAAA
 AGTGGCTGGTGGCTGCTGATTTGGACAGCACAGAAAAAGATTTCCATCACCACAGAAAGGTC
 GGCTGGCAGCACTGGCCAAAGGTGATGGGGTGTGCTACACAGTGATGTGCTACTGGTGTAGTGGA
 TGGAGTTTACTGTTTGTGGAATAAAACGCTGTTTCCGTGGAAAAA

FIGURE 238

MPLALLVLLLLGPGGWCLAEPDRSLREELVITPLPSGDVAATFQFRTRWDSELQREGVSHY
 RLFPKALGQLISKYSLRELHLSFTQGFWRTRYWGPPFLQAPSGAELWVWFQDVTVDKSWK
 ELSNVLSGIFCASLNFIDSTNTVTPTASFKPLGLANDTDHYFLRYAVLPREVVCTENLTPWK
 KLLPCSSKAGLSVLLKADRLFHTSYHSQAVHIRPVCNRACTSISWELRQTL SVVFD AFITG
 QGKKDWSLFRMFSRTLTEPCPLASESRVYVDITTYNQDNETLEVHPPPTTTYQDVILGTRKT
 YAIYDLLDTAMINNSRNLNIQLKWKRPENEAPPVPFLHAQRYVSGYGLQKGELSTLLYNTH
 PYRAFPVLLLDTPWYLRLYVHTLTITISKGKENKPSYIHYQPAQDRLQPHLLEMLIQLPANS
 VTKVSIQFERALLKWTEYTPDPNHGFYVSPSVLSALVPSMVAAPVDWEESPLFNSLFPVSD
 GSNYFVRLYTEPLLVLNLTPTDFSMYPYVNICLTCTVVAVCYGSFYNNLTTRTFHIEEPRTGGLA
 KRLANLIRRARGVPPL

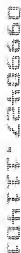


FIGURE 239

CAACATGGGGTCCAGCAGCTTCTTGGTCCTCATGGTGTCTCTCGTTCTTGTGACCCTGGTGG
 CTGTGGAAGGAGTTAAAGAGGGTATAGAGAAAGCAGGGGTTTGCCACAGCTGACAACGTACGC
 TGCTTCAAGTCCGATCCTCCCCAGTGTACACAGACCAGGACTGTCTGGGGGAAAGGAAGTG
 TTGTTACCTGCACTGTGGCTTCAAGTGTGTGATTCTGTGAAGGAAGTGAAGAAGGAGGAA
 ACAAGGATGAAGATGTGTCAAGGCCATACCTGAGCCAGGATGGGAGGCCAAGTGTCAGGC
 TCCTCCTCTACCAGGTGTCTCAGAAATGAATGCTGGGTCTTTCTACCTCTGGGGGTCACTC
 TCACTTGGCACCTGCCCCTGAGGGTCTTGAGACTTGGAATATGGAAGAAGCAATACCCAACC
 CCACCAAAGAAAACCTGAGCTTGAAGTCCTTTCCCCAAAAGAGGGAAGAGTCAAAAAAG
 TCCAGACCCCAGGGACGGTACTTCCCTCTCTACCTGGTGTCTCTCCCTAATGCTCATGAAT
 GGACCCCTCATGAATGAAACCAGTGCCCTTATAAGAGACCCCAAAGAGCTGCCTTGCCCTTC
 TGCAATGTGTGATCACAGCTAGAAGGCACTGTGAGAGAAGAGAAACTGGTCTCACCAGATG
 CTGAATCTGCTGGTGCCTTGATCTTGACTTCCAGCCTCTAGAACTGTAAGAAATAAATAT
 TTGCTGTTTATAATCCAA



FIGURE 240

MGSSSFLVLMVSLVLVTLVAVEGVKEGIEKAGVCPADNVRCFKSDPPQCHTDQDCLGERKCC
YLHCGFKCVIPVKELEEKGKDEDVSRPYPEPGWEAKCPGSSSTRCPQK

Signal sequence:

amino acids 1-19

N-myristoylation sites:

amino acids 23-29, 27-33, 32-38, 102-108

WAP-type 'four-disulfide core' domain signature:

amino acids 49-63

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AAACTCAGCACTTGCGGAGTGGCTCATTGTTAAGACAAAGGGTGTGCACTTCTCGCCAGG
AAACCTCGAGCGGTGAGACTCCGAGTCCGCTACATCAAGGCCCCAGGACATGCAGAACCTTCC
TCTAGAACCACCGACCCACCA**ATG**AGGTTCTGCTCTGTGGATGACGAGCACTGAGCCAAAG
CGTCCAGTGGTCTCTGCTTCTGGCTGTCTGTGTTCTTCTTCTCTGCTTGGCTTGCCTCTTTTA
TTAAGGAGCTCTCAAAACAAGGCTTCCAGGACTCAACCGACAGAGAACAATTAAAGAAAGGCT
CTACAGTCCCTGGCAAAGCCTAAGTCCCGAGCACCCCAAGGGCGAGGAGACAACCATCTA
TGCAGAGCCAGGCCGACAGGACAACATGCCCTCAACACACAAACCCAGGCCAGGCCACACCC
CCGGAAGACAGAGGAAGGAGGACCCAAACAGGCACCGCGGAGGACGAGCAAGGTGCCCA
ACAGACAGAGGCGAGCATGGAAGAGCCAGAAAAGAGAAAACCATTGGTGAAACACACTGT
ACCCAGAGGCGAAGATCGAGGAGTGGCTCTGGCAGGACAGGCGACAATCATGGAAGAGCC
AGGACACAAGACGACCCAAAGGAATTGGGGCCAGACAGGAAGCTCAGCGCTCCAGGACG
GTGTGACAGAAGACCCAGGGCAAGCGGCCAACACAGCCAAAGACGCTTATTCTGCCAAAGATCA
GCACAGAATGCTGGCTCCACAGGAGCAGTGTCAACAAGGACGAGACAGAAAGGATGACCA
CAGCAGTCACTCCCACTTAAGGAAGAAGAACTCAGGCCACCCCAACCCCTTGCCTCTTCCAG
AGCCCCAGCAGCAGAGAAACCAAGACTGAAGCGCCCACTTCAAATCTGAGGCTCCGGT
GGATTTTGAGGAAAAATACAGCTTCAAAATAGGAGGCTCTCAGACAGCTTGCCTTGACTCT
TGAAGATCAAAAGCTCCAAGTTCGCTGTGGTCTCAGAAACTCTTTCTGCCCACTCTCACTCTC
TTCTCGGACTCCAGACTACTCAACCAAGTGAGTGTAGTGGACCGCTTGAACATTTGCACACC
CTTTGGCTTCATGGAGCTCACTACTCTTGGTGCAGAAGGTCGTGACACGCTTCCCTCCAG
TGCCCGCAGCAGCTGCTCTCGGCCAGCTCCCGCTTGGGAGCTCCCGTGCATCACTGCT
CCGCTGGTGGGCAACGGGGCTCTCGAACTCCACATGGGCAGGAGATGACAGCTCA
CGACTAGTGGTCCGAATTGAGCGAGCTCTATTAAAGGCTACGAACAGGATGTGGGCAAT
GGACATCCTTCTACGGCTTTACCGCTTCTCCCTGAACAGCTCACTCTTATATTGGGCAAT
CGGGGTTTCAAGAACGTGCCCTCTTGGGAAGGACGTCCGCTACTTGCACTTCTCGGAAGGCAC
CCGGGACTATGAGTGGCTTGAAGACTGCTTATGAATCAGACGGTGATGCAAAAACCTTT
TCTGGTTCAGGCACAGCCCCAGGAAGCTTTTCCGGAAGCCTTGCACTGACAGCGGTACCTG
TTGCTGCCAACCAAGCTTTCTCCGATACATGAAGAACAGGTTTCTGAGGCTTAAGCCCTGGA
TGGTGCCACTTGAGGATATACGCCCCACCCTCGGGCGCTTCTGCTGCTCACTGCCCTTT
AGCTCTGTGACCAGGTGAGTGCTTATGGCTTCACTACTGAGGGCCATGAGCGCTTTTCTGAT
CACTTACTATGATACATCAAGGAAGCGGCTGATCTTTATACATAACCACTGACTTCAAGCTGGA
GAGAGAAGTCTGAAGCGGCTACAGTACAGGAAGGATAACCGGCTGACACGCTCCGCTG
CCGGAAGCTGCCAAAGCAAGAAG**AGA**CCGGGGCCAGGCGTGCCATGGTCTCTTGGCTGCTC
CAAGGCACAGGATACAGTGGGAATCTTGAGACTTTGGCCATTTCCCATGGCTCAGACTAA
GCTCCAAGCCCTTCAGGAGTTTCAAGGGGAACCTTGAACCATGGAACAAGACTCTCTCAAGAT
GGCAAAATGGCTAATTGAGGTTCTGAGGTTCTTCACTAGTACTGCTGTAGGTTCTGAGGCCAG
GATTTTAAATTAATGGGGTGATGGGTGGCCCAATACCAAACTTCTGCTGAAAACACTGT
CCAGTCCAAAAGCTTCTTGATACAGAAAAAGAACTGGATTTACAGAAACATAAGATCTG
GTTTGAATCCAGATCGAGTTTACAGTTGTGAAGCTTTGAAGGTATTACCTAATCTCACTAC
AGATTGCTAGAAAGCTTTTACGAGTTATCTGATTTAGAAAGGCTCTATACTTGCTCTCTG
TCTTTAAGCTATTTGCAACCTCACTAGCTGTGTAGAAAACGTAAATTACATAAATGATTGTT
GTCCATGGAAGAGCAATAAATTTTCTACAGTCAAAAAAATAAAAAA

FIGURE 242

MRSCLWRCRHLSQGVQWSLLLAFLVFFLFALPSFIKEPQTKPSRHQRTENIKERSLQSLAKP
 KSQAPTRARRTTIYAEPAPENNALNTQTQPKAHTTGDRGKEANQAPPEEQDKVPHTAQRAAW
 KSPEKEKTMVNTLSPRGQDAGMASGRTEAQSWSQDQTKTTQGNNGGQTRKLTASRTVSEKHQ
 KAATTAKTLIPKSHRMLAPTGAIVSTRTRQKGVTTAVIPPKKKPPQATPPAPFQSPTTQRN
 QRLKAANFKSEPRWDFEEKYSFEIGGLQTTCPDSVKIKASKSLWLQKLFLENLTLFLDSRHF
 NQSEWDRLEHFAPPPGFMEELNYSLVQKVVTFRPPVPPQQLLASLPAGSLRCITCAVVGNGG
 ILNNSHMGQEIDSHDYVFRLSGALIKGYEQDVGTRTSFYGFATAFSLTQSLILGNRGFKNVP
 LGKDVRYLHFLEGRDYEWLEALLMNQTVMSKNLFWFRHRPQEAFAREALHMDRYLLHPDFL
 RYMKNRFLRSKTLGDAHWRIRPTTGALLLLTALQLCDQVSAYGFITEGHERFSDHYDTSW
 KRLIFYINHDFKLEREVWKRLHDEGIIRLYQRPGFGTAKAKN

Cytoplasmic Domain:

amino acids 1-10

Type II Transmembrane Domain:

amino acids 11-35

Lumenal catalytic Domain:

amino acids 36-600

Ribonucleotide Reductase small subunit Signature:

amino acids 481-496

N-glycosylation Sites:

amino acids 300-303, 311-314, 331-334, 375-378, 460-463

FIGURE 243

CGATGCGCGGACCCGGGCACCCCCTCCTCCTGGGGCTGCTGCTGGTGCTGGGGCCTTCGCCG
GAGCAGCGAGTGGAATTTGTTCTCGAGATCTGAGGATGAAGGACAAGTTTCTAAAACACCT
TACAGGCCCTCTTTATTTTAGTCCAAAGTGCAGCAAACACTTCCATAGACTTTATACAACA
CCAGAGACTGCACCATTCCTGCATACTATAAAAGATGCGCCAGGCTTCTTACCCGGCTGGCT
GTCAGTCCAGTGTGCATGGAGGATAAGTTGAGCAGACCGGTACAGGAGCAGCACACCAGGAGCC
ATGAGAAGTGCCTTGGAACCAACAGGGAACAGAACTATCTTTATACACATCCCCTCATGG
ACAAGAGATTATTTTTCAGACAGACTCTTCCATAAGTCCTTTGAGTTTGTATGTTGTTG
ACAGTTTGCAATATATATTCGATAAATCAGTGTACTTGACAGTGTTATCTGTCACTTATTT



FIGURE 244

MRGPGHPLLLGLLLVLGSPSEQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFRLYHNT
RDCTIPAYYKRCARLLTRLAVSPVCMEK

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FIGURE 245

GGGCTGGGCCCCCGCGCAGCTCCAGCTGGCCGGCTTGGTCCTGCGGTCCCTTCTCTGGGAGG
 CCCGACCCCGGCGCGCCAGCCCCACCATGCCCCGCGGGGCTCCGCCGGGCGCGCGCG
 CTCACCGCAATCGCTCTGTTGGTGCTGGGGGCTCCCCTGGTGCTGGCCGGCGAGGACTGCCCT
 GTGGTACCTGGACCGGAATGGCTCCTGGCATCCGGGGTTAACTGCGAGTTCTTCACCTTCT
 GCTGCGGGACCTGCTACCATCGGTACTGCTGCAGGGACCTGACCTTGCTTATCACCAGAGG
 CAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGCCTCAGCTGTGAT
 CCTCTTTGTTGCTGTGGTTGCCACCACCATCTGCTGCTTCCTCTGTTCTGTGTGCTACCTGT
 ACCGCCGGCGCCAGCAGCTCCAGAGCCCATTGAAGGCCAGGAGATTCCAATGACAGGCATC
 CCAGTGCAGCCAGTATACCCATACCCCCAGGACCCCAAAGCTGGCCCTGCACCCCCACAGCC
 TGGCTTCATGTACCCACCTAGTGGTCCTGCTCCCCAATATCCACTCTACCCAGCTGGGCCCC
 CAGTCTACAACCTGCAGTCTCCTCCTATATGCCACCACAGCCCTCTTACCCGGGAGCC
 TGAAGGAACCAGCCATGTCTCTGCTGCCCTTCAGTGATGCCAACCTTGGGAGATGCCCTCAT
 CCTGTACCTGCATCTGGTCCTGGGGGTGGCAGGAGTCTCCAGCCACCAGGCCCCAGACCAA
 GCCAAGCCCTGGGCCCTACTGGGGACAGAGCCCCAGGGAAGTGAACAGAGCTGAACCTAGA
 ACTATGAGGGGTGGGGGGAGGGCTTGAATTATGGGCTATTTTTACTGGGGGCAAGGGAGG
 GAGATGACAGCCTGGGTCAAGTGCCTGTTTTCAATAGTCCCTCTGCTCCCAAGATCCCAG
 CCAGGAAGGCTGGGGCCCTACTGTTTGTCCCTCTGGGCTGGGGTGGGGGGAGGGAGGAGGT
 TCCGTCAGCAGCTGGCAGTAGCCCTCCTCTCTGGCTGCCCCACTGGCCACATCTCTGGCCTG
 CTAGATTAAAGCTGTAAAGACAAAA

FIGURE 246

MPPAGLRRAAPLTAIALLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCCGTCYHRYC
CRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCFLCSCCYLYRRRQQLQSP
FEGQEIPMTGIPVQPVYPYPQDPKAGPAPPQPGFMYPSPGPAPQYPLYPAGPPVYNPAAPP
YMPPQPSYPGA

Transmembrane Domains:

amino acids 10-28, 85-110

N-glycosylation Site:

amino acids 38-41

N-myristoylation Sites:

amino acids 5-10, 88-93

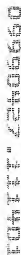


FIGURE 247

GGGGGAGCTAGGCCGGCGGCAGTGGTGGTGGCGGGCGCAAGGGTGAAGGCGGGCCAGAA
 CCCCAGGTAGCTAGAGCAAGAAGATGCTGTTTCTGCCCTCAAAATGGTCCCTTGC AACCATG
 TCATTTCTACTTTCTCTACTGTTGGCTCTCTTAAGTGTGTCCACTCTCTACATGGTGTGAGAG
 CACTGAAGCATCTCAAAACGCTAGTGATGGGACACCATTTCTGTGGAATAAAATACGACTTCT
 CTGAGTACGTCACTCCAGTTTCAATATGATCTCTTGTATCCATGCAAAACCTTACCACGCTGACC
 TTTCTGGGGAACCAACAGTAGAATAACACAGCCAGTCAAGCCACAGCACCATTATCTCTGCA
 TAGTCACCACTGAGATATCTAGGGCCACCTCAGGAAGGGAGCTGGAGAGAGGGCTATCGG
 AAGAACCCCTGAGGCTCTGGAAACACCCCTCAGGAGCAAAATTGCACTGCTGGCTCCCGAG
 CCCCTCCTTTGCGGCTCCCTACACAGTTGTCTATCTACTATGCTGGCAATTCTTTCGGAGAC
 TTTCCACGGATTTTACAAAAGCACTACAGAACCAAGGAAGGGAACTGAGGATACTAGCAT
 CAACACAATTTGAACCCACTGCAGCTAGAAATGGCTTTTCCCTGCTTTTGTATGAACCTGCTCTC
 AAAGCAAGTTTCTCAATCAAAATTAGAAGAGAGCCAAAGGCACCTAGCCATCTCCAATATGCC
 ATTGGTGAATCTGTGACTGTTGCTGAAGGACCTCATAGAAGACATTTTTGTATGTCACGTGGA
 AGATGAGCAGCTATCTGGTGGCTTTCATCATTTTCAGATTTTGTAGTCTGTCAGCAGAGATAACC
 AAGAGTGGAGTCAAGGTTCTGTTTATGCTGTGCGCAGACAGATAAATCAAGCAGGATATGCC
 ACTGGATGCTGCGGTGACTCTCTAGAATTTTATGAGGATTTTTCAGCATACGATATCTCCG
 TACCCAAACAAGATCTTGCTGCTATTCCCGACTTTCAGTCTGGTGTATGGAAAACTGGGGA
 CTGACAACATATAGAAATCTGCTCTGTTTGTGATGCAGAAAAGCTTCTGCAATCAAGTAA
 GCTTTGGCATCAGAGTACTGTGGCCCATGAAGTGCACACAGTGGTTTGGGAACTGGTCA
 CTATGGAATGTTGGAATGATCTTTGGCTAAATGAAGGATTTGCCAATTTTGAAGATTTTGTG
 TCTGTCAAGTGGACCATCTGAACCTGAAGTTGAGATTTTCTTCTTCAAAATGTTTGA
 CGCAATGGAGTAGATGCTTTAAATTTCTCACACCTGTGTCTACCTGTGGAAATCTGCT
 CTCAGATCCGGGAGATGTTTGTATGATGTTTCTTATGATAAGGAGCTTGTATTTCTGAATATG
 CTAAGGGAGTATCTTAGCGCTCAGCGATTTAAAAGTTGGTATTTCTACAGTATCTCCGCAAGCA
 TAGCTATAAAAAACAAAAAACGAGGACCTCTGGATAGTATGGCAAGTATTTGCCCTCAG
 ATGGTGTAAAAGGATGGATGGCTTTTGTCTAGAAGTCAACATCTCATCTTCTATCTCCACAT
 TGGCATCAGGAAGGGTGGATGCTGAACCAATGATGAACACTTGGACACTGCAGAGGGGTTT
 TCCCTCTAACCATCAAGTGAAGGGGGAGGAATGTACACATGAAGCAAGACGACTCATGATGA
 AGGGCTTACGGCGGCGCCGGACACTGGGTACCTGTGGCATGTTCATTTGACATTTATCACC
 AGCAAAATCCAACATGCTCCATCGATTTTGTCTAAAAACAAAAACAGATGTGCTCATCTCCG
 AGAAGAGGTGGAAATGGATCAAAATTTAATGTGGGCATGAATGGCTATTACATTTGCAATACG
 AGGATGATGGATGGGACTCTTTGACTGGCTTTTAAAAGGAACACACAGCAGCTCAGCAGT
 AATGATCGGGCAAGTCTCATTAAACATGCAATTCAGCTCGTCAGCATTTGGGAAGCTGTCCAT
 TGAAGGGGCTTGGATTTATCCCTGTACTTGAACATGAAACTGAAATTTAGCCCGTGTTC
 AAGGTTTGAATGAGCTGATTCCTATGTATAAGTTAATGGAGAAAAGAGATATGAATGAAGT
 GAAACTCAATTCAGGCGCTTCTCATCAGGCTGCTAAGGGAGCTCTATGATAAGCAGACATG
 GACAGACAGGGCTCAGTCTCAGAGCAAAATGCTGCGGAGTGAACACTACTCTCTCGCTGTG
 TGCACAACTATCAGCGCTGCTACAGAGGGCAGAAAGGCTATTTCAAGAAAGTGGAGGAATCC
 AATGGAAACTTGAAGCTGCGTCTCGAGCTGACCTTGGCAGTGTGTTGCTGTGGGGGCCAGAG
 CACAGAAAGGCTGGGATTTTCTTATAGTAAATATCAGTTTCTTGTCCAGTACTGAGAAAT
 GCCAAATTTGAATTTGCCCTCTGCAGAACCCAAAAATAAGGAAAACCTCAATGGCTACTAGAT
 GAAAGCTTTAAGGAGATTAATAAAAAAATCAGGAGTTTCCACAAATCTTACACTATTGG
 CAGGAACCCAGTAGGATACCCACTGGCTGGCAATTTCTGAGGAAAACCTTGAACAACTTG
 TACAAAAGTTTGAATTTGGCTCATCTTCCATAGCCACATGGTAAATGGGTACACAAATCAA
 TTCTCCACAAGACCGCTTGAAGAGGTAAAGGATTTCTCAGCTCTTTGAAAGAAAATGG
 TTCTCAGCTCGTTTGTGTCCAACAGACAATTGAACCAATTTGAAGAAAACATCGGTGGATGG
 ATAGAATTTGTATAAATCAGAGTGTGGTGCAGAAAGTGAAGGATTTGAAGCTATGTGAAAA
 TTCTCTCCTTGGCCGGTTTCTGTTATCTCTAATCACCACATTTTGTGTAGTGTATTTTCAA
 ACTAGAGATGGCTGTTTTGGCTCCAAGTGGAGTACTTTTTTCCCTTCAAGCTATTTTGTGA
 CTATCCCTGTGAAAAGATAAGCTGTGTAGTTTTCATGAATGGGCTTTTTCATGAATGGGCTA
 TCGCTACCATGTGTTTTGTTTCTATCAGAGTGTGTGCCCTGCAACGTAAACCAAGCTGTTGGGT
 TCCTTGCCACAGAAGATAAAGTACCTTATTCTTCTCAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 248

MVFLPLKWSLATMSFLLSSLLALLTVSTPSWCQSTEASPKRSDGTPFPWNKIRLPEYVIPVH
 YDLLIHANLTLTTFWGTTKVEITASQPTSTIILSHHLQISRATLRKGAGERLSEEPLOVLE
 HPPOEQIALLAPEPLLVGLPYTVVIHYAGNLSETFHGFYKSTYRTKEGELRILASTQFEPTA
 ARMAFPFCFDEPAFKASFSIKIRREPRHLAISNMPLVKSVTVAEGLIEDHFDVTVKMSTYLVLA
 FIISDFESVSKITKSGVKVSVYAVDPKINQADYALDAAVTLLEFYEDYFSIPYPLPKQDLAA
 IPDFQSGAMENWGLTTYRESALLFDAEKSSASSKLGITVTVVAHELAHQWFGNLVTMEWWNDL
 WLNEGFAKFMFVSVSVTHPELKVGDYFFGKCFDAMEVDALNSSHPVSTPVENPAQIREMFD
 DVSYDKGACILNMLREYLSADAFKSGIVQYLQKHSYKNTKNEDLWDSMASICPTDGVKGMGDG
 FCSRSQHSSSSSHHQEGVDVKTMMNTWTLQRGFPLITITVRGRNVHMKQEHYMKGSDGAPD
 TGYLWHVPLTFITSKSNMVHRFLKTKTDVLILPEEVEWIKFNVGMNGYIYVHYEDDGWDSL
 TGLLKGTHTAVSSNDRASLINNAFQLVSIGKLSIEKALDLSLYLKHETEMPVFQGLNELIP
 MYKLMEKRDMEVETQFKAFILRLRLDIDKQWTWDEGSVSEQMLRSELLLACVHNYQPCV
 QRAEGYFRKWKESNGNLSLPVDVTLAVFAVGAQSTEGWDFLYSKYQFSLSTEKSQIEFALC
 RTQNKEKLQWLLDESFKGDKIKTQEFQIILTILGRNPVGYPLAWQFLRNWNKLVQKFELGS
 SSIAHVMVMTTNQFSTRRLLEEVGKGFSSSLKENGSQLRCVQQTETIETIENIGWMDKNFDKIR
 VWLQSEKLERM

Signal peptide:

amino acids 1-34

N-glycosylation sites:

amino acids 70-74, 154-158, 414-418, 760-764, 901-905

Neutral zinc metalloproteinases, zinc-binding region signature:

amino acids 350-360

FIGURE 249

CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTTCATCCTCCAC
 TGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCC
 GACCTACCCGGCAATGGACCCCTAAGAACCAGCTGCGACAGCGGCTTGGGTGCCAGGA
 CACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGG
 AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCGGCTCTCCCTGATC
 TCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT
 TTGGGCCCCACAGCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGTCTATGG
 AAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACTGTTATGAT
 GGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC
 CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCCGTGGGTATGACTGAGA
 ACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGACCACCATTATGACACACGGAAC
 TTGGCTCAAGAACCACCTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGT
 GTGTGAGGAGACGCTGCTGCTCATAGATGTAGGACTCAGATCAACCTTGGTGGGGACAAAAG
 GCTGCAGCACTGTTGGGGCTCAAAATTCCAGAAGACCACCATCCACTCAGCCCCCTCCTGGG
 GTGCTTGTGGCCTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG
 CAGCGTTCTGCTGAACCTCCCTCCCTCCTCAAGCTGCCCTGTCCCAGGAGACCGGCAGTGTCT
 CTACCTGTGTGCAGCCCCCTTGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCCCAGG
 GCGCCACTCATTGTTATGATGGGTACATTATCTCTCAGGAGGTGGGCTGTCCACCAAAAT
 GAGCATTCAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTGTAACCACACAGACAAATCG
 GGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGT
 GGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTG
 GTGGGGAGTGGTTTGCCCTTCTGCTTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGA
 CCACCCCACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTTC
 CCATTCTGTCCATGAATCATCTTCCCACACACAATCATTATCTACTCACCTAACAGCA
 AACTGGGGAGAGCCTGGAGCATCCGACTTGGCCTATGGGAGAGGGGACGCTGGAGGAGTG
 GCTGCATGTATCTGATAATACAGACCTGTCCTTTCA

FIGURE 250

MSAVLLLALLGFILPLPGVQALLCQFGTVQHVKVSDLPQWTPKNTSCDSGLGCQDTLMLI
ESGPQVSLVLSKGCTEAKDQEPVTEHRMGFGLSISYTFVCRQEDFCNNLVNSLPLWAPQP
PADPGSLRCPVCLSMEGCLEGTTEEICPKGTHCYDGLRLRGGGIFSNLRVQGCMPQPGCN
LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTSTNTEMCEVGQVCQETL
LLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDL CNSASSSSVLLN
SLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGC
VAQPSSFLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLES LTWGVGLALAPALWWGVVC
PSC

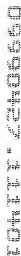


FIGURE 251

GCGACGGGCAGGACGCCCCGTTTCGCCTAGCGCGTGCTCAGGAGTTGGTGTCTCGCTGCGCT
 CAGG**ATG**AGGGGGAATCTGGCCCTGGTGGGCGTTCTAATCAGCCTGGCCTTCTCTGTCACTGCTG
 CCATCTGGACATCCTCAGCCGGCTGGCGATGACGCCTGCTCTGTGCAGATCCTCGTCCCTGG
 CCTCAAAGGGGATGCGGGAGAGAAGGGAGACAAAGGCGCCCCGGGACGGCCTGGAAGAGTCG
 GCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAGTGTGGGTGCTCAT
 GGAAAAATTTGGTCCCATTGGCTCTAAAGGTGAGAAAGGAGATTCCGGTGACATAGGACCCCC
 TGGTCCTAATGGAGAACCAGGCCTCCCATGTGAGTGCAGCCAGCTGCGCAAGGCCATCGGGG
 AGATGGACAACCAGGTCTCTCAGCTGACCAGCGAGCTCAAGTTCATCAAGAATGCTGTGCGC
 GGTGTGCGCGAGACGGAGAGCAAGATCTACCTGCTGGTGAAGGAGGAGAAGCGCTACGCGGA
 CGCCACAGTGTCTTGCAGGGCCGCGGGGACCGCTGAGCATGCCAAGGACGAGGCTGCCA
 ATGGCCTGATGGCCGCATACCTGGCGCAAGCCGGCCTGGCCCGTGTCTTATCGGCATCAAC
 GACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGACCACTCCCCATGCGGACCTTCAACAA
 GTGGCGCAGCGGTGAGCCCAACAAATGCCTACGACGAGGAGGACTGCGTGGAGATGGTGGCCT
 CGGGCGGCTGGAACGACGTGGCCTGCCACACCACCATGTACTTCATGTGTGAGTTTGACAAG
 GAGAACATG**TGA**CGCCTCAGGCTGGGGCTGCCCATTGGGGGCCCCACATGTCCCTGCGAGGGTT
 GGCAGGGACAGAGCCAGACCATGGTGCCAGCCAGGGAGCTGTCCCTCTGTGAAGGGTGGAG
 GCTCACTGAGTAGAGGGCTGTGTCTAAACTGAGAAAATGGCCTATGCTTAAGAGGAAAATG
 AAAGTGTTCCTGGGGTGTGTCTCTGAAGAAGCAGAGTTTCATTACCTGTATTGTAGCCCCA
 ATGTCAATTATGTAATTATTACCCAGAATTGCTCTTCATAAAGCTTGTGCCTTTGTCCAAGC
 TATACAATAAAATCTTTAAGTAGTGCAAGTAAAGTCCAAAAAAAAAAAAAAAAAAAA

FIGURE 252

M R G N L A L V G V L I S I A F L S L L P S G H P Q P A G D D A C S V Q I L V P G L K G D A G E K G D K G A P G R P G R V G
P T G E K G D M G D K G Q K G S V G R H G K I G P I G S K G E K G D S G D I G P P G P N G E P G L P C E C S Q L R K A I G E
M D N Q V S Q L T S E L K F I K N A V A G V R E T E S K I Y L L V K E E K R Y A D A Q L S C Q G R G G T L S M P K D E A A N
G L M A A Y L A Q A G L A R V F I G I N D L E K E G A F V Y S D H S P M R T F N K W R S G E P N N A Y D E E D C V E M V A S
G G W N D V A C H T T M Y F M C E F D K E N M

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FIGURE 253

AGTGACTGCAGCCTTCCTAGATCCCCCTCCACTCGGTTTCTCTCTTTGCAGGAGCACCGGCAG
 CACCAGTGTGTGAGGGGAGCAGGCAGCGGTCCCTAGCCAGTTCTCTTGATCCTGCCAGACCACC
 CAGCCCCCGGCACAGAGCTGCTCCACAGGCACCATGAGGATCATGCTGCTATTACAGCCAT
 CCTGGCCTTCAGCCTAGCTCAGAGCTTTGGGGCTGCTCTGTAAGGAGCCACAGGAGGAGGTGG
 TTCTTGCGGGGGCCGAGCAAGAGGGATCCAGATCTCTACCAGCTGCTCCAGAGACTCTTC
 AAAAGCCACTCATCTCTGGAGGGATTGCTCAAAGCCCTGAGCCAGGCTAGCACAGATCCTAA
 GGAATCAACATCTCCCGAGAAACGTGACATGCATGACTTCTTTGTGGGACTTATGGGCAAGA
 GGAGCGTCCAGCCAGAGGGAAAGACAGGACCTTTCTTACCTTCAGTGAGGGTTCTCGGCC
 CTTTCATCCCAATCAGCTTGGATCCACAGGAAAGTCTTCCCTGGGAACAGAGGAGCAGAGACC
 TTTATAAGACTCTCTACGGATGTGAATCAAGAGAACGTCCCAGCTTTGGCATCCTCAAGT
 ATCCCCCGAGAGCAGAATAGGTACTCCACTTCCGGACTCCTGGACTGCATTAGGAAGACCTC
 TTTCCCTGTCCCAATCCCCAGGTGCGCACGCTCCTGTTACCTTTCTCTCCCTGTTCTTGT
 AACATTCTTGTGCTTTGACTCCTTCTCCATCTTTTCTACCTGACCCTGGTGTGAAACTGCA
 TAGTGAATATCCCCAACCCCAATGGGCATTGACTGTAGAATACCCTAGAGTTCTGTAGTGT
 CCTACATTAATAATATAATGTCTCTCTATTCTCAACAATAAAGATTTTTCATATGAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 254

MRIMLLFTAILAFSLAQSFQAVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGLLK
ALSQASTDPKESTSPEKRDMDHDFVGLMGKRSVQPEGKTGPFLPSVRVPRPLHPNQLGSTGK
SSLGTEEQRPL

Important features:**Signal peptide:**

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 36-45

N-myristoylation site.

amino acids 33-39, 59-65

Amidation site.

amino acids 90-94

Leucine zipper pattern.

amino acids 43-65

Tachykinin family signature.

amino acids 86-92

FIGURE 255

GGGCGTCTCCGGCTGCTCCTATTGAGCTGTCTGCTCGCTGTGCCCGCTGTGCCTGCTGTGCC
 CGCGCTGTGCGCGCTGCTACCGCGTCTGCTGGACGCGGGAGACGCCAGCGAGCTGGTGATTG
 GAGCCCTGCGGAGAGCTCAAGCGCCAGCTCTGCCCGAGGAGCCAGGCTGCCCGTGAGTCT
 CCATAGTTGCTGACGAGAGTGGAGCCATGAGCTGCGTCTCGGGTGGTGTCTATCCCCCTGGGGC
 TGCTGTTCTTGGTCTGCGGATCCCAAGGCTACCTCCTGCCCAACGTCACCTCTTAGAGGAG
 CTGCTCAGCAAATACCAGCACACGAGTCTCACTCCCGGGTCCGCAGAGCCATCCCCAGGGA
 GGACAAGGAGGAGATCCTCATGCTGCACAACAAGCTTCGGGGCCAGGTGCAGCCTCAGGCCCT
 CCAACATGGAGTACATGGTGAGCGCCGGCTCCGGCCGCAGAGGCTGGCACCGGGGGTGGGGC
 CTGGGCCACCGCTGCTCTGTTCCCCAGCCAGCTCTGTTCCCCAGCCAGTGCCTGTGATGG
 CTGGCTCAGGGTCTCCTCTGGCAGGGGAGGATCCCGGCTCTGTTCTGTTTTGTTTGTGTTT
 TTGAGACAGGGTCTCACTCTGCCACTGACGCTGGAGTGCAATGGCACAATCGTCATGCCCTG
 AACCTTAGACTCCCGGGGTTAAGCGATCCTGCTTCAGCCTCCCAAGTAGCTGGAACCTACAG
 GCATGCACCATGGTGCCAGCTAGATTTTAAATATTTTGTGGAGATGGGGTCTTGCTACGT
 TGCCAGGCTGGTCTTGAAGTCTTAGGCTCAAGCAATCCTCCTGCCTCAGCCTCTCAAAGTG
 CTAGGATTATAGGCATGAGTACCCTGCTCTGGCTCTGGCTCTGTTCTTAACATTCTGCCAAA
 ACAACACACGTGGGTTCCTCTGTGCAGAGCCTGCCTCGTTGCCTTCATGTCACTCTTGGTAGC
 TCCACTGGGAACACAGCTCTCAGCCTTTCCACCTGGAGGCAGAGTGGGGAGGGGCCAGGG
 CTGGGCTTTGCTGATGCTGATCTCAGCTGTGCCACACGCTAGCTGCACCACCCTGACTTCTC
 CTTAGCCCGTGTGAGCCTCACTTTCACCTTGGAGAGTCTCTCCTCGCGTGGTTGCCATGACT
 GTGAGATAAGTCGAGGCTGTGAAGGGCCCGGCACAGACTGACCTGCCTCCCCAACCCCTAGG
 CTTTGCTAACCGGGAAAGGAGCTAACGGTGACAGAAGACAGCCAAGGTCAACCTCCCGGGT
 GATTGTGATGGGTGTTCCAGGTGTGGTGGGCGATGCTGCTACTTGACCCCAAGCTCCAGTG
 TGGAAACTTCCTTCTGGCTGGTTTTTCCAGAACTACAGAGGAATGGACCACAGTCTTCCAGG
 GTCCCTCCTCGTCCACCAACCGGGAGCCTCCACCTTGGCCATCCGTGAGCTATGAATGGCTT
 TTTAAACAAACCCAGCTCCAGCCTGGGTAAACATGGTAAAGCCCCGTCTCTACAAAAAATC
 CAAGTTAGCCGGGCATGGTGGTGCGCACCTGTAGTCCAGCTGCAGTGGGACTGAGGTGGAG
 GTGGAGGTGGGGGTGGGAGCTGAGGAAGGAGGATCGCTTGAGCCTGGGAAGTCGAGGCTGC
 AGTGAGCTGAGATTGCACCACTGCACCTCAGCCTGGGTGACAGAGCAAGACCTGTCTCAAAAA

FIGURE 256

MSCVLGGVIPLGLLFLVCGSQGYLLPNVTLLLEELLSKYQHNEHSRVRRAIPREDKEEILML
HNKLRGQVQPQASNMEYMVVSAGSGRRGWHRGWGLGHQPALFPSQLCSPASACDGWLRVSSGR
GGSRLCSVLVFCFETGSHSATDAGVQWHNRHALKP

Important features:**Signal peptide:**

amino acids 1-22

N-glycosylation site.

amino acids 27-31, 41-45

N-myristoylation site.

amino acids 126-132, 140-146

Amidation site.

amino acids 85-89

FIGURE 257

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACT**TATG**GG
GTCTGGGCTGCCCCCTTGTCCTCCTCTGACCCCTCCTTGGCAGCTCACATGGAACAGGGCCGG
GTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGC
TTCCTGGAATTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCTTCAGGGACCAGCGTCAC
CCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA**TGA**CAGCCATTGAAGCCTG
TGTCTTCTTGGCCCGGGCTTTTGGGCCGGGGATGCAGGAGGCAGGCCCCGACCCTGTCTTT
CAGCAGGCCCCACCCTCCTGAGTGGCAATAAATAAAATTCGGTATGCTG



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FIGURE 258

MSGGLPLVLLLTLLGSSHGTGPGMTLQLKLKESFLTNSSESSFLELLEKLCLLLHLPST
VTLHHARSQHHVCNT

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FIGURE 259

AATTGTATCTGTGTAATGTTAAAAACAAACGAAATAAATAGAAAGGAAAACTTTCTGAGTTT
CAAAAACAACAGACTAGTACTCTAAGAACTCTTTAAACAATTAAGTGTAGGATTGCAGT
TATGATTGGATATTATTTAATTCTGTTTCTGATGTGGGGTTCCTCCACTGTGTTCTGTGTGC
TATTAATATTTACCATTGCAGAAGCTTCATTCAGTGTTGAAAATGAATGCTTAGTGGATCTG
TGCCCTTTACGCATATGTTACAAATTATCTGGAGTTCCTAATCAATGCAGAGTCCCCCTCCC
CTCCGATTGTTCTAAATTAATTGAAAGATGTCTGCTGTGGAAAAGGCATGTATTTAAATCTG
TATGATTCTCAACCATCTTTAGTTGGGAAAGGTCCTTGAAAGCCAATGGAAATACTTTTTTT
TTTTCTTGGCACTAATCAAGTGAGTGTTACCTTTTCACTTAGTAGGATGTGTTGTTACGCTA
GTAAAATAGAAACCTGTGTTTATTCTCAGGTATTTTAGAAACAACAGCCATCATTTTATTTT
ATGTGTGTGTTCTTGGCTGTATTCAATAATTATATATTTTGGGCTATCAATATTACTTCAT
TCAATATAAATAACAATAGTAGAAGTTGTTTACTTAGATATGCTTTCTAGTTGCATTTTCTC
AGCCTATGTAAGACTACTTTGTTGTAATAGCCTTTGAAATTTACAGTACTGTCTCTCTACTA
TCTTCAGATTACTTGATTCAAATAAACCAATTATGTTTGTAATTGATATTAATAAAACCAGA
ATAAAAGTTCATATCTACCC

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FIGURE 260

MIGYYLILFLMWGSSTVFCVLLIFTIAEASFVENECCLVDLCLLRICYKLSGVPNQCRVPLP
SDCSK

Important features:

Signal peptide:

amino acids 1-29

100
90
80
70
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FIGURE 261

GAGGATTTGCCACAGCAGCGGATAGAGCAGGAGAGCACCACCGGAGCCCTTGAGACATCCTT
 GAGAAGAGCCACAGCATAAGAGACTGCCCTGCTTGGTGTGTTTGCAGG**ATGAT**TGGTGGCCCTT
 CGAGGAGCTTCTGCATTGCTGGTTCCTGCTTCCAGCTTTTCTGCCCCCGCCGAGTGTAC
 CCAGGACCCAGCCATGGTGCATTACATCTACCAGCGCTTTCGAGTCTTGAGCAAGGGCTGG
 AAAAAATGACCCAAGCAACGAGGGGCATACATTCAAGAAATCCAAGAGTTCTCAAAAAATATA
 TCTGTCTATGCTGGGAAGATGTCAGACCTACACAAGTGAGTACAAGAGTGCAAGTGGGTAACTT
 GGCAGTGAAGTGAACGTGCCCAACGGGAGATTGACTACATACAATACCTTCGAGAGGCTG
 ACCAGTGCATCGTATCAGAGGACAAGACACTGGCAGAAATGTTGCTCCAAGAAAGCTGAAGAA
 GAGAAAAAGATCCGGACTCTGCTGAATCCAAGCTGTGACAACATGCTGATGGGCATAAAGTC
 TTTGAAAAATAGTGAAGAAGATGATGGACACACATGGCTCTTGGATGAAAGATGCTGCTATA
 ACTCTCCAAAGGTGTACTTTATTAATTGGATCCAGAAACAACACTGTTTGGGAATTTGCAAAAC
 ATACGGGCATTTCATGGAGGATAACACCAAGCCAGCTCCCCGGGAAGCAAACTCTAACACTTTC
 CTGGCAGGGAACAGGCCAAGTGATCTACAAGGTTTTCTATTTTTCATAACCAAGCAACTT
 CTAATGAGATAATCAAAATAAACCCTGCAGAGAGGAGACTGTGGAAGATCGAATGCTGCTCCCA
 GGAGGGGTAGGCCGAGCATTTGCTTACCAGCACTCCCCCTCAACTTACATTGACCTGGCTGT
 GGTAGGACATGGGCTCTGGGCCATCCACTCTGGGCCAGGCCACCCATAGCCATTGTTGGTCTCA
 CAAAGATTGAGCCGGGCACACTGGGAGTGGAGCAATTCAATGGGATACCCCATGCAAGAGCCAG
 GATGCTGAAGCCTCATCTCTTGTGTGGGTTCTCTATGTGGTCTACAGTACTGGGGGCCA
 GGGCCCTCATCGCATCACCTGCATCTATGATCCACTGGGCACATCAGTGAGGAGGACTTGC
 CCAACTTGTCTTCCCCAAGAGACCAAGAAGTCACTCCATGATCCATTACAACCCAGAGAT
 AAGCAGCTCTATGCTGGAATGAAGGAAACAGATCATTACAACCTCCAGACAAAGAGAAA
 GCTGCCCTCTGAAG**TAA**TGCAATTACAGCTGTGAGAAAGAGCACTGTGGCTTTGGCAGCTGTTCT
 TACAGGACAGTGAGGCTATAGCCCCCTTCACAATATAGTATCCCTCTAATCACACACAGGAAG
 AGTGTGTAGAAGTGAAATACGTATGCCTCCTTTCCCAATGTCACTGCCTTAGGTATCTTC
 CAGAGCTTAGATGAGAGCATATCATCAGGAAGTTTCAACAATGTCCATTACTCCCCCAA
 CCTCTGGCTCTCAAGGATGACCACATTCTGATACAGCCTACTTCAAGCCTTTTGTGTTTACT
 GCTCCCCAGCATTTACTGTAACTCTGCCATCTCCCTCCCACAAATGAGGTTGTATGCCAGC
 CCCATAATATTCACCACTGGCTTTTCTCTCCCTGGCCCTTGTGTAAGCTCTTCCCTCTTTTT
 CAAATGTCTATTGATATTCTCCCATTTTCACTGCCCAACTAAAATATCTATTAATATTTCTTT
 CTTTTCTTTTCTTTTTTTTGGAGCAAGGTCTCACTATGTTGCCAGGCTGGTCTCAAACCTC
 AGAGCTCAAGAGATCCTCCTGCCTCAGCCTCCTAAGTACCTGGGATTACAGGCATGTGCCAC
 CACACCTGGCTTAAAAATACATTTCTTATTGAGGTTTAACTCTAATTTCCGCTAGCCCTGTCT
 CTTCCACTAAGCTTGGTAGATGTAATAATAAAGTGAATAATTAACATTTGAATATCGCTTT
 CCAGGTGTGGAGTGTTTGACATCATTGAATTTCTCGTTTCACTTTTGTGAAACATGCACAAG
 TCTTTACAGCTGCTCATTCTAGAGTTTAGGTGAGTAACACAATTACAAGTGAAGATACAGC
 TAAAAATACTACAATAATCCCATAGTTTTTCCATTGCCCAAGGAAGCATCAAAATAGCATGTTGTT
 TGTTCACCTACTCTTATAGTCAATGCGTTCATCGTTTACAGCCTAAAAATAATAGTCTGTCCC
 TTTAGCCAGTTTTCATGCTGTGCACAAGACCTTTCAATAGGCCCTTTCAAATGATAATTCCTCC
 AGAAAAACAGTCTAAGGGTGAGGACCCCAACTCTAGCCTCCTCTGTCTTGTCTGCTCTGTCTGT
 TTCTCTGTTTCTGCTTTAAATTCATAAAAGTGACACTGAGCAAAAAAAAAAAAAA

FIGURE 262

MMVALRGASALLVLFLLAFLPPPQCTQDPAMVHYIYQRFVLEQGLEKCTQATRAYIQEFQE
FSKNISVMLGRCQTYTSEYKSAVGNLALRVERAQRIDYIQYLREADECIVSEDKTLAEMLL
QEAEEEKKIRTLNASCNMLMGIKSLKIVKMMMDTHGSWMKDAVNSPKVYLLIGSRNNTV
WEFANIRAFMEDNTKPAPRKQILTLWQGTGQVIYKGFLEFFHNQATSNEIIKYNLQKRTVED
RMLLPGGVGRALVYQHSPSTYIDLAVDEHGLWAIHSGPGTHSHLVLTKEFGTLGVEHSWDT
PCRSQDAEASFLLCGVLYVVYSTGGQGPHRITCIYDPLGTISEEDLPNLFPPKRPRSHSMIH
YNPRDKQLYAWNENGNQIIYKLQTKRKLPLK

FIGURE 263

GGGCGCCCCGCTACTCACTAGCTGAGGTGGCAGTGGTTCCACCAAC**ATG**GAGCTCTCGCAGA
 TGTTCGAGGCTCATGGGGCTGTGGGTGTTGCTTGGGCTGCTGGCCCTGATGGCGACGGCGGCG
 GTAGCGCGGGGGTGGCTGCGCGGGGGGAGGAGAGGAGCGGCCGGCCCGCTGCCAAAAGC
 AAATGGATTTCACCTGACAAATCTTCGGGATCCAAGAAGCAGAAACAATATCAGCGGATTTC
 GGAAGGAGAAGCCTCAACAACAACAACCTTACCCACCGCCTCCTGGCTGCAGCTCTGAAGAGC
 CACAGCGGGGAACATATCTTGCATGGACTTTAGCAGCAATGGCAAATACCTGGCTACCTGTGC
 AGATGATCGCACCATCCGCATCTGGAGCACCAAGGACTTCCTGCAGCGAGAGCACCAGCA
 TGAGAGCCAACGTGGAGCTGGACCACGCCACCTTGGTGCCTTCAGCCCTGACTGCAGAGCC
 TTCATCGTCTGGCTGGCCAACGGGGACACCTCCGTGTCTTCAAGATGACCAAGCGGGAGGA
 TGGGGGCTACACCTTCACAGCCACCCAGAGGACTTCCTAAAAAGCACAGGCGCCTGTCA
 TCGACATTGGCATTGCTAACACAGGGAAGTTATCATGACTGCCTCCAGTGACACCACTGTC
 CTCATCTGGAGCCTGAAGGGTCAAGTGTCTTACCATCAACACCAACAGATGAACAACAC
 ACACGCTGTGTATCTCCCTGTGGCAGATTTGTAGCCTCGTGTGGCTTCACCCAGATGTGA
 AGGTTTGGGAAGTCTGCTTTGGAAAGAAGGGGAGTTCAGAGAGGTGGTGCAGCCTTCGAA
 CTAAAGGGCCACTCCGCGGCTGTGCACCTCGTTTGTCTTCCAAACACTACCGAGGATGGC
 TTCTGTCTCCAAGGATGGTACATGGAACCTGTGGGACACAGATGTGGAATACAAGAAGAAGC
 AGGACCCTACTTGTCTGAAGACAGGCCGCTTTGAAGAGGGCGCGGGTGCCGCGCCGTGCCG
 CTGGCCCTCTCCCCAACGCCAGGCTTTGGCCTTGGCCAGTGGCAGTAGTATTATCTACTTA
 CAATACCCGGCGGGGCGAGAAGGAGGAGTGTCTTTGAGCGGGTCCATGGCAGTGTATCGCCA
 ACTTGTCTTTGACATCACTGGCCGCTTTCTGGCCTCCTGTGGGGACCGGGCGGTGCGGCTG
 TTTCAACAACACTCCTGGCCACCGAGCCATGGTGGAGGAGATGCAGGGCCACCTGAAGCGGGC
 CTCACACGAGAGCACCGCCAGAGGCTGCAGCAGCAGCTGACCCAGGCCCAAGAGACCTTGA
 AGAGCCTGGGTGCCCTGAAGA**ACTG**ACTCTGGGAGGGGCCCGCGCAGAGGATTGAGGAGGAG
 GGATCTGGCCTCCTCATGGCACTGTGCCATCTTTCCTCCCAAGGTGGAAGCCTTTCAGAAGG
 AGTCTCCTGGTTTTCTTACTGGTGGCCCTGCTTCTTCCCATTTGAACTACTCTTGTCTACTT
 AGGTCTCTCTCTTCTTGTCTGGCTGTGACTCTTCCCTGACTAGTGCCAAAGGTGCTTTTCTTC
 CTCCCAGGCCCAAGTGGGTGGAATCTGTCCCACTTGGCACTGAGGAGAATGGTAGAGGAGG
 AGGAGAGAGAGAGAGAATGTATTTTGGCCTTGTGGCAGCACTCTCACACCCAAAGAG
 TTTGTAATGTTCCAGAACAACCTAGAGAACACCTGAGTACTAAGCAGCAGTTTTGCAAGGA
 TGGGAGACTGGGATAGCTTCCCATCACAGAATGTGTTCCATCAAAAGACACTAAGGGATT
 TCCTTCTGGGCCTCAGTTCTATTGTGAAGATGGAGAATAATCTCTCTGTGAACTCTTGTGA
 AAGATGATATGAGGCTAAGAGAATATCAAGTCCCCAGGTCTGGAAGAAAAGTAGAAAAGAGT
 AGTACTATTGTCCAATGTCTGAAAGTGGTAAAGTGGGAACCACTGTGCTTTGAAACCAA
 TTAGAACAACATTCTTGGGAAGGCAAGTTTTCTGGGACTTGATCATACATTTTATATGGT
 TGGGACTTCTCTCTTCGGGAGATGATATCTTGTTTAAGGAGACCTCTTTTCAGTTTCATCAAG
 TTCATCAGATATTGAGTGCCCACTGTGCCCCAAATAAATAGCTGGGATTAAAAAA
 AA

FIGURE 264

MELSQMSELMGLSVLLGLLALMATAAVARGWLRAGEERSGRPACQKANGFPPDKSSGSKKQK
QYQRIRKEKPQQHNFTHRLAALKSHSGNISCMDFSSNGKYLATCADDRTIRIWSTKDFLQ
REHRSMRANVELDHATLVRFSPPDCRAFIVWLANGDTLRVFKMTKREDGGYTFTATPEDFPPK
HKAPVIDIGIANTGKFIMTASSDTTVLIWSLKGQVLSTINTNQMNNTHAAVSPCGRFVASC
FTPDVKVWEVCFGKKGEFQEVVRAFELKGHSAAVHSFAFSNDSRRMASVSKDGTWKLWDTDV
EYKKKQDPYLLKTGRFEEAAGAAPCRLALSPNAQVLALASGSSIHLYNTRRGEKEECFERVH
GECIANLSFDITGRFLASCGDRAVRLFHNTPGHRAMVEEMQGHLLKRASNESTRQLRQQQLTQ
AQETLKSLGALKK

Important features:

Signal peptide:

amino acids 1-25

N-glycosylation site.

amino acids 76-80, 92-96, 231-235, 289-293, 378-382, 421-425

Beta-transducin family Trp-Asp repeat protein.

amino acids 30-47, 105-118, 107-119, 203-216, 205-217, 296-308

FIGURE 265

TGGCCTCCCCAGCTTGCCAGGCACAAGGCTGAGCGGGAGGAAGCGAGAGGCATCTAAGCAGG
 CAGTGTTTTGCCTTACCCCCAAGTGACCATGAGAGGTGCCACGCGAGTCTCAATCATGCTCC
 TCCTAGTAACGTGTGTCTGACTGTGCTGTGATCACAGGGGCTGTGAGCGGGATGTCCAGTGT
 GGGGACAGGCACCTGCTGTGCCATCAGCCTGTGGCTTCGAGGGCTGCGGATGTGCACCCCGCT
 GGGGCGGGAAGGCGAGGAGTGCCACCCCGGCAGCCACAAGTCCCCTTCTTCAGGAAACGCA
 AGCACCACACCTGTCTTGCTTGCCCAACCTGCTGTGCTCCAGGTTCCCGGACGGCAGGTAC
 CGCTGCTCCATGGACTTGAAGAACATCAATTTTTAGGCGCTTGCCCTGGTCTCAGGATACCCA
 CCATCCTTTTCTGAGCACAGCCTGGATTTTATTTCTGCCATGAAACCCAGCTCCCATGAC
 TCTCCCAGTCCCTACACTGACTACCCTGATCTCTCTTGTCTAGTACGCACATATGCACACAG
 GCAGACATACCTCCCATCATGACATGGTCCCCAGGCTGGCCTGAGGATGTCACAGCTTGAGG
 CTGTGGTGTGAAAGGTGGCCAGCCTGGTCTCTTCCCTGCTCAGGCTGCCAGAGAGGTGGTA
 AATGGCAGAAAGGACATTCCCCCTCCCCTCCCAGGTGACCTGCTCTCTTCTGGGCCCTG
 CCCCTCTCCCCACATGTATCCCTCGGTCTGAATTAGACATTCTGGGCACAGGCTCTTGGGT
 GCATTGCTCAGAGTCCCAGGTCTTGGCCTGACCCTCAGGCCCTTACGCTGAGGTCTGTGAGG
 ACCAATTGTGGGTAGTTTCATCTTCCCTCGATTGGTTAACTCCTTAGTTTCAGACCACAGAC
 TCAAGATTGGCTCTTCCCAGAGGGCAGCAGACAGTCACCCCCAAGGCAGGTGTAGGGAGCCCA
 GGGAGGCCAATCAGCCCCCTGAAGACTCTGGTCCCAGTCAGCCTGTGGCTTGTGGCCTGTGA
 CCTGTGACCTTCTGCCAGAATTGTCATGCCTCTGAGGCCCCCTCTTACCACACTTTACCAGT
 TAACCACTGAAGCCCCCAATTTCCACAGCTTTTCCATTAAATGCAATGGTGGTGGTTCAA
 TCTAATCTGATATTGACATATTAGAAGGCAATTAGGGTGTTCCTTAAACAACCTCTTTCCA
 AGGATCAGCCCTGAGAGCAGGTGGTGACTTTGAGGAGGGCAGTCCTCTGTCCAGATTGGGG
 TGGGAGCAAGGGACAGGGAGCAGGGGCTGAAAGGGGCACTGATTTCAGACCAGGGGAGG
 CAACTACACACCAACATGCTGGCTTTAGAATAAAAGCACCAACTGAAAAA

FIGURE 266

MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGECHP
GSHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF

Signal peptide:

amino acids 1-19

Tyrosine kinase phosphorylation site:

amino acids 88-95

N-myristoylation sites:

amino acids 33-39, 35-41, 46-52

FIGURE 267

AGCGCCCGGGCGTCGGGGCGGTAAAAGGCCGGCAGAAAGGAGGCACTTGAGAAATGCTCTTTC
 CTCCAGGACCAAGTTTCTTACCATGGGGATGTGGTCCATTGGTGCAGGAGCCCTGGGGGC
 TGCTGGCTTGGCATTGCTGCTTGCCAAACACAGAGCTGTTTCTGTCCAAGCCCCAGAAAGCGG
 CCCTGGAGTACCTGGAGGATATAGACCTGAAAACTGGAGAAGGAACCAAGGACTTTCAAA
 GCAAAGGAGCTATGGGAAAAAATGGAGCTGTGATTATGGCCGTGCGGAGGCCAGGCTGTTT
 CCTCTGTGAGAGGAAGCTGCGGATCTGTCTCCTGAAAAGCATGTTGGACCAGCTGGGCG
 TCCCCCTCTATGCAGTGGTAAAGGAGCACATCAGGACTGAAGTGAAGGATTTCAGCCTTAT
 TTCAAAGGAGAAATCTTCTGGATGAAAAGAAAAAGTTCTATGGTCCACAAAGGCGGAAGAT
 GATGTTTATGGGATTTATCCGCTCTGGGAGTGTGGTACAACCTTCTTCCGAGCCTGGAACGGAG
 GCTTCTCTGGAACCTGGAAGGAGAAGGCTTCATCCTTGGGGGAGTTTTCGTGGTGGGATCA
 GGAAGCAGGGCATTCTTCTTGAGCACCGAGAAAAAGAATTTGGAGACAAAGTAAACCTACT
 TTTCTGTTCTGGAAGCTGCTAAGATGATCAAACACAGACTTTGGCCTCAGAGAAAAATGAT
 TGTGTGAAACTGCCAGCTCAGGGATAACCAGGGACATTCACCTGTGTTTCATGGGATGTATT
 GTTTCCTCTCGTGTCCCTAAGGAGTGAGAAACCCATTTATACTCTACTCTCAGTATGGATTA
 TTAATGTATTTTAATATTCTGTTTAGGCCCTAAGGCAAAATAGCCCCAAAACAAGACTGA
 CAAAAATCTGAAAACTAATGAGGATTATTAAGCTAAAACCTGGGAAATAGGAGGCTTAAAA
 TTGACTGCCAGGCTGGGTGCAGTGGCTCACACCTGTAATCCAGCACTTTGGGAGGCCAAGG
 TGAGCAAGTCACTTGAAGTCGGGAGTTCGAGACCAGCCTGAGCAACATGGCGAAACCCCGTC
 TCTACTAAAAATACAAAAATCACCCGGGTGTGGTGGCAGGCACCTGTAGTCCAGCTACCCG
 GGAGGCTTGAGGCAGGAGAATCACTTGAACCTGGGAGGTGGAGGTTGCGGTGAGCTGAGATCA
 CACCACGTATTCCAGCCTGGGTGACTGAGACTCTAACTAA

FIGURE 268

MSFLQDPSFFTGMWSIGAGALGAAALALLLANTDVFLSKPQKALEYLEDIDLKTTLEKEPR
TFKAKELWEKNGAVIMAVRRPGCFLCREEADLSSLKSMQLDQGVPLYAVVKEHIRTEVKDF
QPYFKGEIFLDEKKKFYGFQRRKMMFMGFIRLGWYNFFRAWNGGFSGNLEGEFILGGVFV
VGSGKQGILLEHREKEFGDKVNLLSVLEAAKMIKPQTLEASEK

268/330
TFKAKELWEKNGAVIMAVRRPGCFLCREEADLSSLKSMQLDQGVPLYAVVKEHIRTEVKDF
QPYFKGEIFLDEKKKFYGFQRRKMMFMGFIRLGWYNFFRAWNGGFSGNLEGEFILGGVFV
VGSGKQGILLEHREKEFGDKVNLLSVLEAAKMIKPQTLEASEK

FIGURE 269

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCC
 GGCCAGGTGCCCCGTCGCAGGTGCCCCCTGGCCGGAGATGCGGTAGGAGGGGCGAGCGCGAGA
 AGCCCCCTCCTCGGCGCTGCCAACC CGCACCCAGCCC ATGGC GAACCCGGGCTGGGGCTG
 CTTC TGGCGCTGGGCCTGCCGTTCCTGCTGGCCGCTGGGGCCGAGCCTGGGGGCAAATACA
 GACCACTTCTGCAAATGAGAATAGCACTGTTTTGCCTTCATCCACCAGCTCCAGCTCCGATG
 GCAACCTGCGTCCGGAAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCTTG
 CTCCTGGCTGTGGGGCTGGCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGG
 CACCTACCGGCCAGTAGCGAGGAGCAGTTCTCCCATGCAGCCAGGCCCGGGCCCCCTCAGG
 ACTCCAAGGAGACGGTG CAGGGCTGCCTGCCATC TAGGTCCCCTCTCCTGCATCTGTCTCC
 CTTCA TTGCTGTGTGACCTTGGGGAAAGGCAGTGCCCTCTCTGGGCAGTCAGATCCACCCAG
 TGCTTAATAGCAGGGAAGAAGGTACTTCAAAGACTCTGCCCTGAGGTCAAGAGAGGATGGG
 GCTATTCACTTTTATATATTTATATAAAATTAGTAGTGAATGAAAAAAAAAAAAAAAAAAAA

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FIGURE 270

MANPGLGLLLALGLPFLLARWGRAWGQIQTTSANENSTVLPSTSSSSDGNLRPEAITAIIV
VFSLLAALLLAVGLALLVRKLRKRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

MANPGLGLLLALGLPFLLARWGRAWGQIQTTSANENSTVLPSTSSSSDGNLRPEAITAIIV
VFSLLAALLLAVGLALLVRKLRKRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

FIGURE 271

AATATATCATCTATTTATCATTAATCAATAATGTATTCTTTATTCCAATAACATTTGGGTT
TTGGGATTTTAATTTTCAAACACAGCAGAAATGACATTTTTCTGTCACATATTATTATTGTTG
GTATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTACTTTCT
ATCAAGAAATAAAGAGAACCACAGTCAACCCACACAATCATCTTTAGAAGACAGTGTGACTC
CTACCAAAGCTGTCAAACCACAGGCAAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGA
GGGTTAATTCTTGGTGCTGAAGCCTGGGGCAGGGGTGTAAAGAAAAAACTTAGATTCAATG
ATTGTAAATTTAAGGCAAATACACATATTAGTATTACCTTAGTGTAAATGTATCCCTGTCATA
TATACAATAAGGTGAAATTATAAGTACCCTATGCAGTTGGCTGGACAGTTCTAAATTGGACT
TTATTAATTTTAAAAATCAGTAACTGATTTATCACTGGCTATGTGCTTAGATCTACAGGAGA
TCATATAATTTGATACAAATAAAAGAAAAGTGTCTCTCCCTTACAGAATTGACATTTTAA
ATGCGATACAGTTAGAATAGGAAATATGACATTAGAAAGGAAGAATGACAGGGAGAAAGGAA
AGAAGGGAAAATGTTGCCAAGGAAAAAAAAA

FIGURE 272

MTFFLSLLLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGK
GIVKGRNLDSRGLILGAEAWGRGVKKNT

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FIGURE 274

MGLFRGFVFLVLCLLHQSNSTSFIKLNNNGFEDIVIVIDPSVPEDEKIIIEQIEDMVTASTY
 LFEATEKRFFFKNVSILIPENWKENPQYKRPKHENHKKHADVIVAPPTLPGRDEPYTKQFTEC
 GEKGEYIHFTPDLLLGKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATR
 CSAGISGRNRVYKCGGSCLSRACRIDSTTKLYGKDCQFFPDKVQTEKASIMFMQSIDSVVE
 FCNEKTHNQEAPSLQNIKCNFRSTWEVISNSEDFKNTIPMVTPPPPPVFSLKISQRIVCLV
 LDKSGSMGGKDRNLNRMNQAAKHFLQITVENGSWVGVMVHFDSTATIVNKLIQIKSSDERNTLM
 AGLPTYPLGGTSICSGIKYAFQVIGELHSQLDGEVLLLTGDGEDNTASSCIDEVKQSGAIVH
 FIALGRAADEAVIEMSKITGGSHFYVSDEAQNNGLIDAFGALTSGNTDLSQKSLQLESKGLT
 LNSNAWMNDTVIIDSTVGKDTFFLITWNSLPPSISLWDPSTIMENFTVDATSKMAYLSIPG
 TAKVGTWAYNLQAKANPETLTITVTSRAANSSVPPITVNAKMNKDVNSFPSPMIVYAEILQG
 YVPVLGANVTAFIESQNGHTEVLELLDNGAGADSFKNDBGVYSRYFTAYTENGRYSLKVRAG
 GANTARILKLRPPLNRAAYIPGWVVNGEIEANPPRPEIDEDTQTTLDEFSRTASGAFVVSQV
 PSLPLPDQYPPSQITDLDTVHEDKIIILTWTAPGDNFVGVKQRYIIRISASILDRLDSFDD
 ALQVNTTDLSPKEANSKESFAFKPENISEENATHIFIAIKSIDKSNLTSKVSNIAQVTLFIP
 QANPDIDPTPTPTPTPTPKSHNSGVNISTLVLSVIGSVVIVNFIISTTI

Signal peptide:

amino acids 1-21

Putative transmembrane domains:

amino acids 284-300, 617-633

Leucine zipper pattern.

amino acids 469-491, 476-498

N-glycosylation site.amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,
628-632, 811-815, 832-836, 837-841, 852-856, 896-900

CTCTAGGTGGAAACCTGGGGATAGATTACTTCAGCAAAAGCCGGAAAGACATACGTCGCCG
GGCAGGGGTGAACAACAGTGTATCTTTTGTATCTGCTGTGGCTCGTCTTATTCAGGAAGA
ACCGCAAGGTAAATTTTGACCACAGGAGCAATGATGATGCCAATCTCTCAATCTCCCTTCTGAACC
CCAGTTATGCGAGGATTTACTAGAGAGTCACTCAACACCAAGAGCGGCTCTTCGGCTTAACCT
GTGGTTGGAGGAGAACCTTTGTGGGGTCGCTTCTTACAGCTGCTCGAAGTGACTTGCTCTGA
GGGTGGACAGAGAAAGAAAGAGTCCCTCTGCTGTGTGCTGCACATCAGGAGGCTGTATGAGG
AATGAAGGTGAAATCTGGAGATTTCACTTCAGTCACTGCTTCTGCTCGCAAGTGAATCTTTAAAA
GTAGAGAAGTCTGCTGTGTGTGTAACTCAAGAGGCAAGTCTGTCTAGAGAAGAAATGGATG
CAAGCAGCTCCGGGGGGCCCCAACCGATGCTTCTGTGTGCTAGCCGGGAAGCGTTCCTGTGGG
GGCCGGCTTTTGGAGGATCCACCGGTTTGGACAGCATGGCTGATCTGATGATGATGTTTGGG
GGGGGCTGTTTGGTGATTTTCCGGGTTGGTGGTTTGTGCTGGTGTCTCTGTGTGCTATCTCTGT
CTGTACATGTTTGGCTGCACCCAAAAGGTGACGAGGAGAGCTGGCAATCGCCAGGGGCCAACAG
CTCACGGGAAGAGGGGCTCACCGGCGCTCTCTCAGGAGTGGGAGGAGCAGCCAGCACTAGCTGA
TCAGCAACAGCGCGCATCTCAACCTCTCAAGAGGAGCTCGAGAGAGAGTGAAGCAGTCAGAA
TGCTGAGTGAATCTGAGAGGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG
GGCCAGCTCTGCGCTTCTTGCACTCGCAGGTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG
CCACAGAGTATCGACAGTCTCTTTCAGTCTTACTCTACAGAAAGTGTGACCTCTGGACATCG
CAATCCGCCCAACCCGAGGAGAAGCTTGTAGGAAGAGCAGAAGCGGATGAGTTGGTGAACCACTT
GAATCAGCTTTGGAGAGCTGAACAACTCTGCAGAGAAGCCCAATCCAGTCTCTACCGCCT
CTGATTTTCATAGAAGGATTCACCAAGCAGAAGGAGCAAAAGGACATGTATGAGCTCACCTCAA
AGGGGACCAAAACCAAGTAATCAACAGCGCTCATCTATTTCGACATTTCAGCCCATCATGAAGT
AAAAATGAAAGACTCAACATCTGGCCAAACCGCTTATCAATGTATTACGTGCCCTACGAAAAAGGGT
ACAAGTTCCGGCAGTTCATGAGAAATTCAGGAGATGTGCATGAGCAGATGGAGAGCTCAATCT
CACTGTTGTTACTTTGGGAAAGAAAGAAATCAAGTGAAGTGAAGAAATCTGGAAAAACCTTCCAAA
GCTGCCAAATCTCAGAACTTTACCTTTCATCCAGTGAATGGAAGATTTCTCGGAAAGAGGAATG
ATGTTTGAGGCGCGCTCTTGGAAAGGGAAGCAAGCTCCTCTCTTTTCTTTTCTGAGCATCTACTT
TCAGCAAGTCACTCAACAGTGTAGCTGAATCAACAGCCAGGGAAGAGATTTATTCAGTTT
CTTTTCAGCAGCACTCAACAGTGTGAGTCTGATCCACAGCTGAGTCTGCTTTTCTGAGCAG
AGCTGCTCATAAAGAGGAACAGCGATTTTGAGAGATTTGGATTTTGGAGCTCTTCTGAGCAGT
TCAGACTTCATCAATATAGTGGTGGTTTATCTGACATCAAAAGCTGGGCGAGGAGTGTGCAC
CTTTTTCGCAAGTATCTCCACAGCAACTCATATGTGTCAGGACGCTTGGCAGACTCTTCCACC
CTTGGCATGAGAAGCGCTGCATGACAGAGTGCACCCCGAGCAGTCAAGATGTGCATGAGTCCAA
GGCCATGAACGAGCATCCACCGGCAGTGGGCTGCTGTGTTTCAGGCACAGATAGAGGCTCAC
CTTTCGCAACAGAAAGAGCAAGACAGTGTACAAAATAACAGCACTCCAGAGAGAAGTGTGGGAGA
CACTTTTCTTCTTCTTGTCAATTAATCGAAGTGGCTGCAACAGAGAAAGACTTCCATAAAGGAC
ACAAAAGAAATGGACTGATGGTGACAGATGAGAAGAACTCGAATTTCTCTCTGTGGCTTTTAC
AACAGAAATCAAAATCTCCGCTTTAGGCTTGCAAAAGTAACCCAGTTGACCTGTGAAGTGTCTGACA
AAGGCAAGATGCTTGTGAGATTAAGCTTAAGTGTGGAGGTTTGAATGTGTTTACAATACAT
GAGACCTGTTGTTTGTGTGCTGATTTGAATATCATGATTTAAGACAGTTTGTGAATAAATTCAT
TAGCATGAAGGCGAAGCATTTCTCTCAATATGAATGAGCTATCAGCAGGCGCTAGTTTCTGAG
TATGATGATGAGTGAAGGAGGAGGAGGATAGGCTATATGATACAGTGAATGATGATCAATAAGT
AAATTAATGAGCAGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG
AAAAATATCTGCTTCTTTGTGTGCTCTTTAACTGCTCGTTTCTTTCTTTCTTTTCTTTAAAT
GCATCTTTTCTCCCTGTGATTTATAGTCTGCTTTTAAATTAACCTTTGCAAGCTTACAGAGA
GCAAGTGTGGCCTACATTTTATATTTTAAAGAAGACTTTGAGATGCATATGAGAATTTCA
GTTCAAGATCAAAATGTATGCCATCTCAAGGACATGCCAAATGCTGATTTCTGTCAGGCATGAT
TCAGGACTTGAGACATAGGAAGGAATGTTTGTATATACAGACGTACAGATAGTTTCTCTGAA
GAGTATTTTGAAGGAGGACATGAACACTGGAGGAAGAGAAATGACACTTCTGCTTTTACAGAA
AAGGAACACTCTCAGACTGGTGATATCTGTGATACCTAAAGTACGAAACCACTTCTTCTCTCA
GAGTAGGGGCGGCTTTCTTCACTGTTTAAATAAACCAATATACCGTGTGAACCAACAACTCTCT
TTTCAAAAAGGGGTGCTCTCTCGCTTCTGCTTCCAGTAAGAAGAAATGGAAGAAAAATATATAT
ATATATATATATTTGGAAGATCAATCATCTGCCAGATCTAGTGGGATGGAAGTTTGTGTCATAC
GCTATCCACCCGAGGCGGTGGAAGTAACGTAAATTTTAAATTAAGCAGTCTTACTCAATCA
CTGCT
ACATGAGTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
CTTTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
GCTTGGTGTGTGTAAGAAATGATTTGATTTGATCTGCTGATGTTTGAATTTAATTAAGAAAC
AGGCTCATGATGGAAGTGGTATTTGACAGCAATAAAATATGATTTGTGATATGAA

FIGURE 276

MMMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQALALPRANSFTGKEGYQAVLQ
EWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFL
HSQVDKAEVNAGVKLATEYAAVFFDSFTLQKVYQLETGLTRHPPEKPVVRKDKRDELVEAIES
ALETLNNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSP
MKVKNEKLNMAANTLINIVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVK
GILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTR
LNTQPGKKVFYFVLFQYNPGIIYGHHDVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFI
NIGGFDLDIKGWGGEDVHLYRKYLSNLIVVRTPVRLFHLWHEKRCMDELTPQYKMCMQS
KAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSSKKT



FIGURE 277

GAAAGA**ATG**TTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACCTGTGCAACC
 AGGTGCAGAAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCAT
 ATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA
 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCTACTTTGCAATGTAACCCAGAGGGT
 ATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCCTGCTGTTGAGGTGC
 AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAACCT
 CTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCATCTG
 GATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTAT
 CAGGGATCTGGCAACGTAGAAGAAAGAACAAGAACCATCTGAAGTGGATGACGCTGAAGAT
 AAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCCCTGGACATGAAGGG
 GGGCATATTAATGATGCCTTCA**TGAC**CAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGT
 TGTTCTGCTTCTCAAGAAATTAACATTTGTTTCTGTGTGACTGCTGAGCATCCTGAAATA
 CCAAGAGCAGATCATATATTTTGTTCACCATTCTTCTTTGTAATAAAATTTTGAATGTGCT
 TGAAAGTGAAAAGCAATCAATTATACCCACCAACACCCTGAAATCATAAGCTATTCACGAC
 TCAAAATATTCTAAATATTTTTCTGACAGTATAGTGTATAAATGTGGTCATGTGGTATTTG
 TAGTTATTGATTTAAGCATTTTGTAGAAATAAGATCAGGCATATGTATATATTTTCACACTTC
 AAAGACCTAAGGAAAAATAAAATTTCCAGTGGAGAATACATATAATATGGTGTAGAAATCAT
 TGAAAATGGATCCTTTTGGACGATCACTTATATCACTCTGTATATGACTAAGTAAACAAAAG
 TGAGAAGTAATTATTGTAAATGGATGGATAAAAAATGGAATTACTCATATACAGGGTGAATT
 TTATCCTGTTATCACACCAACAGTTGATTATATATTTTCTGAATATCAGCCCCCTAATAGGAC
 AATTCTATTTGTTGACCATTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAG
 TAATAATCATCTCTTTTTAAAAA

FIGURE 278

MLWLLFFLVTAIHAE LCQPGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRKVP
NREATEISHVLLCNVTQRVSEFWFVVTDP SKNHTLP AVEVQSAIRMNKNRINNAFFLNDQTLE
FLKIPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRRKKNKEPSEVDDAEDKC
ENMITIENGIPSDPLDMKGGILMMPS



FIGURE 279

AACTCAAACCTCCTCTCTCTGGGAAAACGCGGTGCTTGCTCCTCCCGGAGTGGCCTTGGCAGG
 GTGTTGGAGCCCTCGGTCTGCCCGTCCGGTCTCTGGGGCCAAGGCTGGGTTTCCCTC**ATGT**
 ATGGCAAGAGCTCTACTCGTGCGGTGCTTCTTCTCCTTGGCATACAGCTCACAGCTCTTTGG
 CCTATAGCAGCTGTGGAATTTATACCTCCCGGTGCTGGAGGCTGTTAATGGGACAGATGC
 TCGGTTAAATGCACTTTCTCCAGCTTTGCCCTGTGGGTGATGCTTAACAGTGACCTGGA
 ATTTTCGTCTCTAGACGGGGACCTGAGCAGTTTGTATTCTACTACCACATAGATCCCTTC
 CAACCCATGAGTGGGCGGTTTAAGGACCGGGTGTCTTGGGATGGGAATCCTGAGCGGTACGA
 TGCCTCCATCCTTCTCTGGAACTGCAGTTCGACGACAATGGGACATACACCTGCCAGGTGA
 AGAACCACCTGATGTTGATGGGGTGATAGGGGAGATCCGGCTCAGCGTCGTGCACACTGTA
 CGCTTCTCTGAGATCCACTTCTTGCTCTGGCCATTGGCTCTGCCTGTGCACTGATGATCAT
 AATAGTAATGTAGTGGTCTCTTCCAGCATTACCGGAAAAAGCGATGGGCCGAAAGAGCTC
 ATAAAGTGGTGGAGATAAAATCAAAAGAAGAGGAAAGGCTCAACCAAGAGAAAAAGTCTCT
 GTTTATTTAGAAGACACAGAC**TAA**CAATTTAGATGGAAGCTGAGATGATTTCCAAGAACAA
 GAACCCTAGTATTTCTTGAAGTTAATGGAACTTTCTTTTGCTTTTCCAGTTGTGACCCGT
 TTTCCAACCAAGTTCTGCAGCATATTAGATTCTAGACAAGCAACACCCCTCTGGAGCCAGCAC
 AGTGCTCCTCCATATCACCAGTCATACACAGCCTCATTATTAAGGTCTTATTTAATTTTCA
 GTGTAAATTTTTCAAGTGCTCATTAGGTTTTATAACAAGAAGCTACATTTTTGCCCTTAA
 GACACTACTTACAGTGTTATGACTTGTATACACATATATTGGTATCAAAGGGGATAAAAGCC
 AATTTGTCTGTTACATTTCCCTTTCAGTATTTCTTTTAGCAGCACTTCTGCTACTAAAGTTA
 ATGTGTTTACTCTCTTTCCTTCCCACATTCTCAATTAAGGTGAGCTAAGCCTCCTCGGTG
 TTTCTGATTAACAGTAAATCCTAAATTCAACTGTTAAATGACATTTTATTTTATGTCTC
 TCCTTAACTATGAGACACATCTTGTTTTACTGAATTTCTTTCAATATTCAGGTGATAGATT
 TTTGTCG

FIGURE 280

MYGKSSTRAVLLLLLGIQLTALWPAAVEIYTSRVLEAVNGTDARLKCTFSSFAPVGDALTVT
 WNFRLDGGPEQFVFYYHIDPFQPMSEGRFKDRVSWDGNPERYDASILLWKLQFDDNGTYTCQ
 VKNPPDVGVIIEIRLSVVHTVRFSEIHFLALAIGSACALMIIVIVVVLFQHYRKKRWAER
 AHKVVEIKSKEEERLNQEKVSVYLEDTD

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ACTCTTGGGAGTTTCCATCTTTCTGGTCTCTGCCAGAATCCGACAACAGCTGCTCCAGCTG
ACACGTATCCAGTACTGGTCTCTGCTGATGATGAAGCCCTGATGCTGAAACCACTGCTGCT
GCAACCACTGCGACCACTGCTGCTCTACCACTGCAACCACCGCTGCTTCTACCACTGCTCG
TAAAGACATTCCAGTTTACCCAAATGGGTTGGGGATCTCCCGAATGGTAGAGTGTGTCCCT**T**
GAGATGGAATCAGCTTGAGTCTTCTGCAATTGGTCACAACTATTATGCTTCCTGTGATTTC
ATCCAACCTACTTACCTTGCTACGATATCCCTTTATCTCTAATCAGTTTATTTCTTTCAA
ATAAAAAATAACTATGAGCAACATAAAAAAAAAAAAAA

FIGURE 283

GGACTCTGAAGGTCCCAAGCAGCTGCTGAGGCCCCCAAGGAAGTGGTTCCAACCTTGGACCC
 CTAGGGGTCTGGATTGCTGGTTACAAGATAACCTGAGGGCAGGACCCCATAGGGGA**AATGC**
 TACCTCCTGCCCTTCCACCTGCCCTGGTGTTCACGGTGGCCTGGTCCCTCCTTGCCGAGAGA
 GTGTCTGGGTTCAGGGACGCAGAGGACGCTCACAGACTCCAGCCCTTTGTTACCGAGAGGAC
 ACTTGGCAAGGTCCAGCGATGGTCCGGAGTCCACACACAGACTGGCGGCAGGGCAGGAGGGG
 GACAGTTCTGTGTGCTTGGTTGGACAGTAAGAGGGTCTTGGCCAGTCCAGGGTGGGGGGCG
 GC**AA**ACTCCATA**AA**GAACCAGAGGGTCTGGGCCCCGGCCACAGAGTCATCTGCCAGCTCCT
 CTGCTGCTGGCCAGTGGGAGTGGCACGAGGTGGGGCTTTGTGCCAGT**TAA**AAACCACAGGCTGG
 ATTTGCCTGCGGGCCATGGTCCCTGTCTAGGGCAGCAATTCTCAACCTTCTTGCTCTCAGGA
 CCCC**AA**AGAGCTTTCATTGTATCTATTGATTTTACCACATTAGCAAT**TA**AAACTGAGAAAT
 GGGCCGGGCACGGTGGCTCACGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCGGGTGGAT
 CACCTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCTTGTCTACT**AAAA**
 TAC**AAAAA**ATTAGCCAGGCACAGTGGTGTGCACCTGGTAGTCCCAGTTACTCGGGAGGCTGAG
 GCAG**GA**AAATCGCTTGAACCCAGGAGGCGGACGTTGCGGTGAGCCGAGATCGCGCCGCTGAT
 TCCAGCCTGGGCGACAAGAGTGAGACTCCATCTCACACA

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FIGURE 284

MLPPALPPALVFTVAWSLLAERVSWVRDAEDAHRLQPFVTERTLGKVQRWSGVHTQTGGRAG
GGQFCCAWLDSKRVLASPGWGAANSIKNQRVWAPATESSAQLCCWFPVGVARGGALCQ

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FIGURE 285

GTCATGCCAGTGCCTGCTCTGTGCCTGCTCTGGGGCCCTGGGCAATGGTGACCGGCCTGCCTCA
 GCGGCCCCCATGGGCGGCCAGAACTGGCACAGCATGAGGAGCTGACCCCTGCTCTTCCATGG
 GACCCCTGCAGCTGGGCCAGGCCCTCAACGGTGTGTACAGGACCACGGAGGGACGGCTGACAA
 AGGCCAGGAACAGCCTGGGTCTCTATGGCCGCACAATAGAACTCCTGGGGCAGGAGGTCAGC
 CGGGGCCGGGATGCAGCCAGGAACCTCGGGCAAGCCTGTTGGAGACTCAGATGGAGGAGGA
 TATTCTGCAGCTGCAGGCAGAGGCCACAGCTGAGGTGCTGGGGGAGGTGGCCCAGGCACAGA
 AGGTGCTACGGGACAGCGTGCAGCGGCTAGAAGTCCAGCTGAGGAGCGCCTGGCTGGGGCCCT
 GCCTACCGAGAATTTGAGGTCTTAAAGGCTCACGCTGACAAGCAGAGCCACATCCTATGGGC
 CCTCACAGGCCACGTGCAGCGGCAGAGGCGGGAGATGGTGGCACAGCAGCATCGGCTGCGAC
 AGATCCAGGAGAGACTCCACACAGCGGCGCTCCCAGCCTGAATCTGCCTGGATGGAAGTCTGAG
 GACCAATCATGCTGCAAGGAACACTCCACGCCCCGTGAGGCCCTGTGCAGGGAGGAGCTG
 CCTGTTCACTGGGATCAGCCAGGGCGCCGGGCCCCACTTCTGAGCACAGAGCAGAGACAGAC
 GCAGGCGGGGACAAAGGCAGAGGATGTAGCCCCATTGGGGAGGGGTGGAGGAAGGACATGTA
 CCCTTTTCATGCCTACACACCCCTCATTAAGCAGAGTCGTGGCATTTCAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAA

FIGURE 286

MPVPALCLLWALAMVTRPASAAPMGGPELAQHEELTLLEHGTLLGQALNGVYRTTEGRLTK
ARNSLGLYGRTELLGQEVSRGRDAAQELRASLLETQMEEDILQLQAEATAEVLGEVAQAQK
VLRDSVQRLEVQLRSAWLGPAYREFEVLKAHADKQSHILWALTGHVQRQRREMVACQHRLRQ
IQERLHTAALPA

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FIGURE 287

GGCAAC**ATG**GCTCAGCAGGCTTGCCCCAGAGCCATGGCAAAGAATGGACTTGTAATTTGCAT
 CCTGGTGATCACCTTACTCCTGGACCAGACCACCAGCCACACATCCAGATTAAAAGCCAGGA
 AGCACAGCAAACGTCGAGTGAGAGACAAGGATGGAGATCTGAAGACTCAAATTTGAAAAGCTC
 TGGACAGAAAGTCAATGCGCTTGAAGGAAATTCAAGCCCTGCAGACAGTCTGTCTCCGAGGCAC
 TAAAGTTCACAAGAAATGCTACCTTGCTTCAGAAGGTTTGAAGCATTTCATGAGGCCAATG
 AAGACTGCATTTCCAAAGGAGGAATCCTGGTTATCCCCAGGAACCTCCGACGAAATCAACGCC
 CTCCAAGACTATGGTAAAAGGAGCCTGCCAGGTGTCATGACTTTTGGCTGGGCATCAATGA
 CATGGTCACGGAAGGCAAGTTTGTGTGACGTCAACGGAATCGTATCTCCTTCTCAACTGGG
 ACCGTGCACAGCCTAACGGTGGCAAGCGAGAAAACCTGTGTCTGTCTCCCAATCAGCTCAG
 GGCAAGTGGAGTGATGAGGCCGTGTCGAGCAGCAAGAGATACATATGCGAGTTCACCATCCC
 TAA**ATAG**GTCTTTCTCCAATGTGTCTCCAAGCAAGATTCATCATAACTTATAGGTTTATGA
 TCTCTAAGATCAAGTAAAATCATAATTTTACTTATTAATAAATTTGCAACACAAGATCAAT
 GTCCATAGCAATATGATAGCATCAGCCAAATTTTGCTAACACATTTCTTTGGGATTTTGCCCT
 TCCTGGGGTATAGGGGATCAGAAATATTGATCCATGTGCACGCAGATAAAATGGCTTCTGCT
 AAACAGACTAAAATCTTTCTCTAGTCTTTCTCACTTGTAACAAACCCAGTTTGTTTTCAA
 AAATCAGTAGCAATGCAACTCATCÂCTCTAGAAAAGCAAGCTTAGGCTACCTGAAGATT
 TTCCCTTGGAAGTTTAGCGTATGTTTGACTAACAAAAATTCCTACATCAGAGACTCTAGGT
 GCTATATAATCCAAAAACTTTTCAGCCTGTTGCTCATCTGTCCCATGCTGGCAATAATACC
 TTGTGAGCCCATTACCCTTATTTTGAATTGCTCCATCTCCTGGTGGGACTGTATCTTGTCT
 GCCATATCAGAACACAAAACCCCTGAAGAGGTTCTGATTGATTTTTTTTTTTTCTTCATGCC
 TACCCTTTTTTTGGAAGTTTCCAGCCGCAATTTGAAATGAAATGACAAGGTGTATATTGAT
 CAATTTTCATTCCCACCATTGCATTACAACCTCTAACTTAAATGGGTAACCCTAAGGCATAT
 CAAAGAAGCAGATTGCATGATAAACGGAATAGAAAAAAGAACCTACATTTATTTTGCTTT
 AGCATCCTTACTCTCACCTTTTATGAGATTGAGAGTGGACTTACATTTCCTTTTTTACATTT
 TCGTATATTTATTTTTTTTAGCCATCATTATATGTTTAAAGTCTATTATGGGCAACCAATCTT
 TGGAAGCTGAAAACCTGAATTTAAAGAATGCTATCTTGGAAAATTGATAGCTCTGTGCAATT
 TTTTATCTGCGCTAGTGCTATTCTGCTTGTTTAACTAGATTGTACAAAATAACTTCATTGCT
 TAATATCAAATTACAAAGTTTAGACTTGAGGGGAAATGGGCTTTTTAGAAAGCAAACAATTTT
 AAATATATTTTGTCTTCAAATAAATAGTGTTTAAACATTGAATGTGTTTTGTGAACAAATAT
 CCCACTTTGCAAACTTTAACTACACATGCTTGGAATTAAGTTTTAGCTGTTTTTCATTGCTCA
 ATAATAAAGCCTGAATTCGTATCAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 288

MAQQACPRAMAKNGLVICILVITLLLDQTTSHTSRLKARKHSKRRVRDKDGD LKTQIEKLWT
EVNALKEIQALQTVCLRGTKVHKKCYLASEGLKHFHEANEDCISKGGILVIPRNSDEINALQ
DYGKRSLPGVNDFWLGINDMVTEGKFVDVNGIAISFLNWDRAQPNGGKRENCVLFSSAQGK
WSDEACRSSKRYICEFTIPK

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FIGURE 289

GCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCGCAGGTTCCCCGCGCGC
CCCGAGCCCCCGCGCCATGAAAGCTCGCCGCCCTCCTGGGGCTCTGCGTGGCCCTGTCCTGCA
GCTCCGCTGCTGCTTTCCTTAGTGGGCTCGGCCAAGCCTGTGGCCAGCCTGTGCTGCGCTG
GAGTCGGCGGCGAGGCCGGGGCCGGGACCTGGCCAACCCCTCGGCACCCTCAACCCGCT
GAAGCTCCTGCTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGT
GTGTGGCTGAGCTGGGTCCCCAGGCCGTGGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGG
GCCCTGACAGTGTTTGGCTGAGCCGAGACTGGAGCATCTACACCTGAGGACAAGACGCTGCC
CACCCGCGAGGGCTGAAAACCCCGCCGCGGGGAGGACCCTCCATCCCCTTCCCCCGGCCCT
CTCAATAAACGTGGTTAAGAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAA

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FIGURE 290

MKLAALLGLCVASCSSAAAFVLGSAKPVAQFVAALESAAEAGAGTLANPLGTINPLKLLLS
SLGIPVNHLEGSQKCV AELGPQAVGAVKALKALLGALT VFG

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FIGURE 291

TGAAGGACTTTTCCAGGACCCAAAGGCCACACACTGGAAGTCTTGCAGCTGAAGGGAGGCAC
 CCTTGGCCTCCGACGCCGATCAC**ATGA**AAGGTGGTGCCAAAGTCTCCTGCTCCTCGTCTCCTCTG
 GCACAGGTGTGGCTGGTACCCGGCTTGGCCCCCAGTCTCAGTCGCCAGAGACCCAGCCCC
 TCAGAACCAGACCAGCAGGGTAGTGCAGGCTCCAGGGAGGAAGAGGAAGATGAGCAGGAGG
 CCAGCGAGGAGAAGGCCGGTGAGGAAGAGAAAGCCTGGCTGATGGCCAGCAGGCAGCAGCTT
 GCCAAGGAGACTTCAAACCTTCGGATTGAGCCTGCTGCCAAAGATCTCCATGAGGCACGATGG
 CAACATGGTCTTCTCTCCATTTGGCATGTCTTTGGCCATGACAGGCTTGATGCTGGGGGCCA
 CAGGGCCGACTGAAACCCAGATCAAGAGAGGGCTCCACTTGACAGGCCCTGAAGCCACCAAG
 CCGGGCTCCTGCCTTCCCTCTTTAAGGGACTCAGAGAGACCCCTCTCCCGCAACCTGGAACT
 GGGCCTCTCACAGGGGAGTTTTGCCTTCATCCACAAGGATTTGATGTCAAAGAGACTTTCT
 TCAATTTATCCAAGAGGTATTTTGATACAGAGTGCGTGCTATGAATTTTCGCAATGCCTCA
 CAGGCCAAAAGGCTCATGAATCATTACATTAACAAAGAGACTCGGGGAAAATTTCCAAACT
 GTTTGATGAGATTAATCTGAAACCAATTAATCTTTGTTGGATTACATCTTGTCAAAGGGA
 AATGGTTGACCCCATTTGACCCGTGTCTTCCCGAAGTCGACACTTTCCACCTGGACAAGTAC
 AAGACCATTAAGGTGCCCATGATGTACGGTGCAGGCAAGTTTGGCTCCACCTTTGACAAGAA
 TTTTCGTTGTCTGTCCTCAAACCTGCCCTACCAAGGAATGCCACCATGCTGGTGGTCTCA
 TGGAGAAAATGGGTGACCACCTCGCCCTTGAAGACTACCTGACCACAGACTTGGTGGAGACA
 TGGCTCAGAAACATGAAACCAGAAACATGGAAGTTTTCTTTCCGAAGTTCAAGCTAGATCA
 GAAGTATGAGATGCATGAGCTGCTTAGGCAGATGGGAATCAGAAGAATCTTCTCACCCTTG
 CTGACCTTAGTGAACCTCTCAGCTACTGGAAGAAATCTCCAAGTATCCAGGGTTTACGAAGA
 ACAGTGATTGAAGTTGATGAAAGGGGCACTGAGGCAGTGGCAGGAATCTGTGCAAGAAATTAC
 TGCTTATTTCCATGCCTCCTGTCTATCAAAGTGGACCGGCCATTTTCATTTCTATGATGATGAAG
 AAACCTCTGGAATGCTTCTGTTTCTGGGCAGGGTGGTGAATCCGACTCTCCTA**TA**ATTGAGG
 ACATGCATAAGCACTTCGTGCTGTAGTAGTGTGAATCTGAGGTATCAACACACACAGGA
 TACCAGCAATGGATGGCAGGGGAGAGTGTTCCTTTTGTCTTAACTAGTTTAGGGTGTCTC
 AAATAAATACAGTAGTCCCACTTATCTGAGGGGGATACATTCAAAGACCCCAAGCAGATGC
 CTGAAACGGTGGACAGTGTGTAACCTTATATATATTTTTTCTACACATACATACCTATGAT
 AAAGTTTAATTTATAAATTAGGCACAGTAAGAGATTAACAATAATAACAACATTAAGTAAAA
 TGAGTTACTTGAACGCAAGCACTGCAATACCATAACAGTCAAACCTGATTATAGAGAAGGCTA
 CTAAGTGACTCATGGCGAGGAGCATAGACAGTGTGGAGACATTGGGCAAGGGGAGAATTCA
 CATCTGGGTGGGACAGACAGGACGATGCAAGATTCATCCCACTACTCAGAAATGGCATGC
 TGTCTAAGACTTTTAGATTGTTTATTTCTGGAATTTTTCATTTAATGTTTTTGACCATGGT
 TGACCATGGTTAACTGAGACTGCAGAAAGCAAAACCATGGATAAGGGAGGACTACTACAAA
 GCATTAATTTGATACATATTTTTTAAAAAAAAAAAAAAAAAAAA

FIGURE 292

MKVVP S L L S V L L A Q V W L V P G L A P S P Q S P E T P A P Q N Q T S R V V Q A P R E E E E D E Q E A S E E K A G E
 E E K A W L M A S R Q Q L A K E T S N F G F S L L R K I S M R H D G N M V F S P F G M S L A M T G L M L G A T G P T E T Q I
 K R G L H L Q A L K P T K P G L L P S L F K G L R E T L S R N L E L G L S Q G S F A F I H K D F D V K E T F F N L S K R Y F
 D T E C V P M N F R N A S Q A K R L M N H Y I N K E T R G K I P K L F D E I N P E T K L I L V D Y I L F K G K W L T P F D P
 V F T E V D T F H L D K Y K T I K V P M Y G A G K F A S T F D K N F R C H V L K L P Y Q G N A T M L V V L M E K M G D H L
 A L E D Y L T T D L V E T W L R N M K T R N M E V F F P K F K L D Q K Y E M H E L L R Q M G I R R I F S P F A D L S E L S A
 T G R N L Q V S R V L R T V I E V D E R G T E A V A G I L S E I T A Y S M P P V I K V D R P F H F M I Y E E T S G M L L F
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CTGGGATCAGCCACTGCAGCTCCCTGAGCACTCTCTACAGAGACGCGGACCCAGAC**ATGAG**
GAGGCTCCTCCTGGTCACCAGCCTGGTGGTTGTGCTGCTGTGGGAGGCAGGTGCAGTCCCAG
CACCCAAGGTCCTTATCAAGATGCAAGTCAAACACTGGCCCTCAGAGCAGGACCCAGAGAAG
GCCTGGGGGCGCCGTGTGGTGGAGCCTCCGGAGAAGGACGACCAGCTGGTGGTGTCTGTTCC
TGTCAGAAAGCCGAAACTCTTTGACACCGAGGAGAAGCCACGAGGTCAGGGCAGGGGCCCA
TCCTTCCAGGCACCAAGGCCTGGATGGAGACCAGGACACCTTGGGCGGTGTCTTGAGTCCC
GAGCCCGACCATGACAGCCTGTACCACCTCCGCTGAGGAGGACCAGGGCGAGGAGAGGCC
CCGGTTGTGGGTGATGCCAAATCACCAGGTGCTCCTGGGACCGGAGGAAGACCAAGACCACA
TCTACCACCCCCAG**TAG**GGCTCCAGGGGCCATCACTGCCCCGCGCCTGTCCCAAGGCCCAGG
CTGTTGGGACTGGGACCTCCCTACCCTGCCCAGCTAGACAAATAAACCCAGCAGGCAAA
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FIGURE 294

MRLLLLVTSLVVVLLWEAGAVPAPKVF IKMQVKHWPSEQDPEKAWGARVVEPPEKDDQLVVL
FPVQKP KLLTTEEKPRGQGRGPILPGTKAWMETEDTLGRVLSPEPDHDSLYHPPFEEDQGEE
RPRLWVMPNHQVLLGPEDQDHIYHPQ

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FIGURE 295

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTG
TACCCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACA**ATGA**ACCAACTCAGCTTCTCTGC
TGTTTCTCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAA
TGGACCTGTTCTTCTGCTCTCCATCTCTGCCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCC
TAGTGCAATTTGATGGCCTGTATTTTCTCCGCACTGAGAATGGTGTTATCTACCAGACCTTCT
GTGACATGACCTCTGGGGGTGGCGGCTGGACCCTGGTGGCCAGCGTGCAATGAGAATGACATG
CGTGGGAAGTGACGGTGGCGGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCC
AGAGGGGGACGGCAACTGGGCCAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCG
ATGACTACAAGAACCCTGGCTACTACGACATCCAGGCCAAGGACCTGGGCATCTGGCACGTG
CCCAATAAGTCCCCCATGCAGCACTGGAGAAACAGCTCCCTGCTGAGGTACCGCACGGACAC
TGGCTTCTCCAGACACTGGGACATAATCTGTTTGGCATCTACCAGAAATATCCAGTGAAAT
ATGGAGAAGGAAAGTGTGGACTGACAACGCCCGGTGATCCCTGTGGTCTATGATTTTGGC
GACGCCCAGAAAAACAGCATCTTATTACTCACCCATATGCCAGCGGGAATTCATGCGGGATT
TGTTCACTTACGGGTATTTAATAACGAGAGAGCAGCCAACGCCCTTGTTGTCTGGAATGAGGG
TCACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAGGATACTTTCCAGAGGCCAGT
CCCCAGCAGTGTGGAGATTTTCTGGTTTTGATTGGAGTGGATATGGAACATCATGTTGGTTA
CAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCGT**TGA**GAGTTTGTG
GGAGGGAACCCAGACCTCTCTCCCAACCATGAGATCCCAAGGATGGAGAACAACCTTACCCA
GTAGCTAGAATGTTAATGGCAGAAGAGAAAAACAATAAATCATATTGACTCAAGAAAAAAA

FIGURE 297

GC GGAGCCGGCGCGGCTGCGCAGAGGAGCCGCTCTCGCCGCCGCCACCTCGGCTGGGAGCC
CACGAGGCTGCCGCATCCTGCCCTCGGAACAATGGGA CTGGCGCGCGAGGTGCTTGGGCCG
CGCTGCTCCTGGGGACGCTGCAGGTGCTAGCGCTGCTGGGGGCCGCCATGAAAGCGCAGCC
ATGGCGGCATCTGCAACATAGAGAATTCTGGGCTTCACACAAC TCCAGTGCTAACTCAAC
AGAGACTCTCCAACATGTGCCTTCTGACCATACAAAATGAAACTTCCAACAGTACTGTGAAAC
CACCAACTTCAGTTGCCTCAGACTCCAGTAATACAACGGTCACCACCATGAAACCTACAGCG
GCATCTAATACAACAACACCAGGGATGGTCTCAACAAATATGACTTCTACCACCTTAAAGTC
TACACCCAAAAACAACAGTGTTTCACAGAACACATCTCAGATATCAACATCCACAATGACCG
TAACCCACAATAGTTCAGTGACATCTGCTGCTTCATCAGTAACAATCACAACAAC TATGCAT
TCTGAAGCAAAGAAAGGATCAAAATTTGATACTGGGAGCTTTGTTGGTGGTATTGTATTAAC
GCTGGGAGTTTTATCTATTCTTTACATTGGATGCAAAATGTATTACTCAAGAAGAGGCATTC
GGTATCGAACCATAGATGAACATGATGCCATCATTTAAGGGAAATCCATGGACCAAGGATGGA
ATACAGATTGATGCTGCCCTATCAATTAAATTTGGTTTATTAATAGTTTAAAACAATATTCT
CTTTTTGAAATAGTATAAACAGGCCATGCATATAATGTACAGTGTATTACGTAAATATGTA
AAGATTCTTCAAGGTAACAAGGTTTTGGGTTTTGAAATAAACATCTGGATCTTATAGACCGT
TCATACAATGGTTTTAGCAAGTTCATAGTAAGACAAACAAGTCCTATCTTTTTTTTTGGCT
GGGGTGGGGCATTTGGTCACATATGACCAGTAATTGAAAGACGTCATCACTGAAAGACAGAA
TGCCATCTGGGCATACAAATAAGAAGTTTGTACAGCACTCAGGATTTTGGGTATCTTTTGT
AGCTCACATAAAGAACTTCAGTGCTTTTCAGAGCTGGATATATCTTAATTACTAATGCCACA
CAGAAATTATACAATCAAACTAGATCTGAAGCATAATTTAAGAAAAACATCAACATTTTTTG
TGCTTTAAACTGTAGTAGTTGGTCTAGAAACAAAATACTCC

FIGURE 298

MGLGARGAWAALLLGTLLQVLALLGAAHESAAMAASANIENSGLPNSSANSTETLQHVPSDH
TNETSNSTVKPPTSVASDSSNTTVTTMKPTAASNTTTPGMVSTNMTSTTLKSTPKTTSVSQN
TSQISTSTMTVTHNSSVTSAASSVTITTTMHSEAKKGSKFDTGSFVGGIVLTLGVLSILYIG
CKMYYSRRGIRYRTIDEHDAI I

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FIGURE 299

CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCCGG
 TCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCAGCGATGCGCACCCTGTGGGAGGC
 CTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTGCTGCCTGGCGCTTTCGGTGTGCTGCTGGC
 GCAGCTGTGACAGCGCCCAAGAATTTCGAGGATGTGAGATGTAATGTATCTGCCCCCT
 ATAAAGAAAATTCGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGATTGCCTT
 CATGTTGTGGAGCCCATGCTGTGCGGGGGCCTGATGTAGAAGCATACTGTCTACGCTGTGA
 ATGCAAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTATAATTTATCTCTCCA
 TTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCATACTGAAGAGG
 CGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTGGGGATCACCAGCCTTT
 TGCAAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCAACGTGCTGAACAAGGTAG
 AATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTCTGCTTTGACCGG
 CATGTTGTCTCAGCTAAATTGGGAATTGAATTCAAGGTGACTAGAAAGAAAACAGGCAGACAA
 CTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATTTTAATACCTTGTTGATTTTACCAACT
 GTTGCTGGAAGATTCAAACTGGAAGCAAAACTTGCTTGATTTTTTTTTCTTGTTAAACGTA
 ATAATAGAGACATTTTTAAAGCACACAGCTCAAAGTCAGCCAATAAGTCTTTTCTATTG
 TGACTTTTACTAATAAAAAATAATCTGCCTGTAATATTCTTGAAGTCCTTTACCTGGAACA
 AGCACTCTCTTTTTACCACATAGTTTTAACTTGACTTTCAAGATAAATTTTCAGGGTTTTTG
 TTGTTGTTGTTTTTGTGTTGTTTTGTTGTTGGTGAGAGGGGAGGGATGCCTGGGAAGTGTT
 AACAACTTTTTCAAGTCACTTTACTAAACAACTTTTGTAATAGACCTTACCTTCTATTT
 TCGAGTTTCATTTATATTTGTCAGTGAGCCAGCCTCATCAAGAGCTGACTTACTCATTTG
 ACTTTTGACAGTACTGTATTTATCTGGGTATCTGCTGTGCTGCACCTCATGGTAACGGGAT
 CTAAATGCCTGGTGGCTTTTCACAAAAGCAGATTTTCTTCACTGTACTGTGATGTCTGATG
 CAATGCATCTAGAACAACTGGCCATTGCTAGTTTACTCTAAAGACTAAACATAGCTTG
 GTGTGTGGTCTTACTCATCTTCTAGTACCTTTAAGGACAAATCTAAGGACTTGGACACT
 TGCAATAAAGAAAATTTATTTAAACCAAGCCTCCCTGGATTGATAATATATACACATTTG
 TCAGCATTTCCGGTCGTGGTGAGAGGCAGCTGTTGAGCTCCAATATGTGCAGCTTTGAACT
 AGGGCTGGGGTGTGGGTGCCTCTCTGAAAGGTCTAACCATTATTGGATAACTGGCCTTTTT
 TCTTCTATGTCTCTTTTGGAAATGTAACAATAAAATAATTTTGAACATCAA

FIGURE 300

MATLWGGLRLGSLLSLSCLALSLLLLAQLSDAAKNFEDVRCKCICPPYKENS GHIYNKNIS
QKDCDCLHVVEPMPVRGPDVEAYCLRCECKYEERSSVTIKVTIIIIYLSILGLLLLYMYLTL
VEPILKRRLFGHQLIQSDDDIGDHQPFANAHDVLA RSRSRANVLNKVEYAQQRWKLQVQEQ
RKSVFDRHVVLS

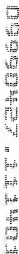


FIGURE 301

GCACCTGCGACCACCGTGAGCAGTCCATGGCGTACTCCACAGTGCAGAGAGTCGCTCTGGCTT
CTGGGCTTGTCCTGGCTCTGTGCTGCTGCTGCCAAGGCCTTCCTGTCCGCGGGAAGCGG
CAGGAGCCGCCGCCGACACCTGAAGGAAAATTGGGCCGATTTCCACCTATGATGCATCATCA
CCAGGCACCTCAGATGGCCAGACTCCTGGGGCTCGTTTCCAGAGGTCTCACCTTGCCGAGG
CATTTGCAAAGGCCAAAGGATCAGGTGGAGGTGCTGGAGGAGGAGGTAGTGAAGAGGTCTG
ATGGGGCAGATTATTCCAATCTACGGTTTTGGGATTTTTTATATATACTGTACATTCTATT
TAAGGTAAGTAGAATCATCCTAATCATATTACATCAATTCAAAATCTAATATGGCGATAAAAA
TCATTGTCTACATTAAAACTTCTTATAGTTCATAAAATTATTTCAAATCCATCATCTCTTTA
AATCCTGCCTCCTCTTCATGAGGTACTTAGGATAGCCATTATTTCAGTTTCACATAAGAATG
TTTACTCAATGTTTAAGTGTTTTGCCCCAAAATTCACTAACAAGGCAGAACTAGGACTT
GAACATGGATCTTTTGGTTCCTAATCCAGTGAGTGATACAATTCAATGCACTCCCCTGCCA

FIGURE 302

MAYSTVQRVALASGLVLALSLLLPKAFLSRGKRQEPPTPEGKLGFRFPPMMHHHQAPSDGQT
PGARFQRSHLAFAKAKGSGGGAGGGGSGRGLMGQIIPYGFIFLYIILFKVSRIILI
ILHQ

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FIGURE 303

CGGCTCGAGTGCAGCTGTGGGGAGATTTCAGTGCATTGCCTCCCCCTGGGTGCTCTTCATCTT
 GGATTGAAAGTTGAGAGCAGC**ATG**TTTTGCCCACTGAAACTCATCCTGCTGCCAGTGTTAC
 TGGATTATTCCTTGGGCCTGAATGACTTGAAATGTTTCCCCGCTGAGCTAACAGTCCATGTG
 GGTGATTCAGCTCTGATGGGATGTGTTTCCAGAGCACAGAAGACAAATGTATATTCAAGAT
 AGACTGGACTCTGTCACCAGGAGAGCACGCCAAGGACGAATATGTGCTATACTATTACTCCA
 ATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCGGTACACTTGATGGGGGACATCTTATGC
 AATGATGGCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGA
 AATCCGCCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGCGGTGGTACTGCATGTGCTTCCAG
 AGGAGCCCAAAGAGCTCATGGTCCATGTGGGTGGATTGATTGATGGGATGTGTTTTCCAG
 AGCACAGAAGTGAAACACGTGACCAAGGTAGAATGGATATTTTCAGGACGGCGCGCAAAGGA
 GGAGATTGTATTTCTGTACTACCACAACTCAGGATGTCTGTGGAGTACTCCAGAGCTGGG
 GCCACTTCCAGAAATCGTGTGAACCTGGTGGGGGACATTTCCGCAATGACGGTTCATCATG
 CTTCAAGGAGTGAGGGAGTCAGATGGAGGAACTACACCTGCGATATCCACCTAGGGAACTT
 GGTGTTCAAGAAAACCATTTGTGCTGCATGTGAGCCCGAAGAGCCTCGAACACTGGTGACCC
 CGGCAGCCCTGAGGCCTCTGGTCTTGGGTGGTAATCAGTTGGTGATCATTGTGGGAATTGTC
 TGTGCCACAATCCTGCTGCTCCCTGTTCTGATATTGATCGTGAAGAAGACCTGTGGAATAA
 GAGTTCAGTGAATTCTACAGTCTTGGTGAAGAACACGAAGAAGACTAATCCAGAGATAAAAG
 AAAAACCCCTGCCATTTTGAAAGATGTGAAGGGGAGAAACACATTTACTCCCCAATAATTGTA
 CGGGAGGTGATCGAGGAAGAAGAACCAAGTGAAAAATCAGAGGCCACCTACATGACCATGCA
 CCCAGTTTGGCCTTCTCTGAGGTGAGATCGGAACAACCTCACTTGAAAAAAGTCAGGTGGGG
 GAATGCCAAAAACACAGCAAGCCTTT**TGA**GAAGAATGGAGAGTCCCTTCATCTCAGCAGCGG
 TGGAGACTCTCTCCTGTGTGTGCTCCTGGGCCACTCTACCAGTGATTTCAGACTCCCCTCTC
 CCAGCTGTCTCCTGTCTCATTGTTTGGTCAATACACTGAAGATGGAGAATTGGAGCCTGG
 CAGAGAGACTGGACAGCTCTGGAGGAACAGGCCTGCTGAGGGGAGGGGAGCATGGACTTGGC
 CTCTGGAGTGGGACACTGGCCCTGGGAACCAGGCTGAGCTGAGTGGCCTCAAACCCCCGTT
 GGATCAGACCCCTCCTGTGGGCAGGGTCTTAGTGGATGAGTTACTGGGAAGATCAGAGATA
 AAAACCAACCCAAATCAA

FIGURE 305

CTATGAAGAAGCTTCCTGGAAAACAATAAGCAAAGGAAAACAAATGTGTCCCATCTCACATG
 GTTCTACCCCTACTAAAGACAGGAAGATCATAAACTGACAGATACTGAAATGTAAGAGTTGG
 AAACCTACATTTTGCAAAGTCATTGAACTCTGAGCTCAGTTGCAGTACTCGGGAAGCC**ATG**CA
 GGATGAAGATGGATACATCACCTTAATATTAAACTCGGAAACCAGCTCTCGTCTCCGTTG
 GCCCTGCATCCTCCTCCTGGTGGCGTGTGATGGCTTTGATTCTGCTGATCCTGTGCGTGGGG
 ATGGTTGTGCGGCTGGTGGCTCTGGGGATTGGTCTGTGCATGCAGCGCAATTACCTACAAGA
 TGAGAATGAAAATCGCACAGGAACCTGCAACAATTAGCAAAGCGCTTCTGTCAATATGTGG
 TAAAACAATCAGAATAAAGGGCACTTTCAAAGGTCATAAATGCAGCCCCGTGACACAAAC
 TGGAGATATTATGGAGATAGCTGCTATGGGTTCTTCAGGCACAACCTAACATGGGAAGAGAG
 TAAGCAGTACTGCACTGACATGAATGCTACTCTCCTGAAGATTGACAACCGGAACATTGTGG
 AGTACATCAAAGCCAGGACTCATTTAATTCGTTGGGTCGGATTATCTCGCCAGAAGTCGAAT
 GAGGTCTGGAAGTGGGAGGATGGCTCGGTTATCTCAGAAAATATGTTTGAGTTTTTGAAGA
 TGGAAAAGGAAATATGAATTGTGCTTATTTTCATAATGGGAAAATGCACCCCTACCTTCTGTG
 AGAACAAAACATTATTTAATGTGTGAGAGGAAGGCTGGCATGACCAAGGTGGACCAACTACCT
TAATGCAAAGAGGTGGACAGGATAACACAGATAAGGGCTTTATTGTACAATAAAAGATATGT
 ATGAATGCATCAGTAGCTGAAAAAAAAAAAAAA

FIGURE 306

MQDEDEGYITLNIKTRKPALVSVGPASSSWVRVMALILLILCVGMVVGLVALGIWSVMQRNYL
QDENENRTGTLQQLAKRFCQYVVKQSELKGTFKGHKCSPCDTNWRYYGDSYGFFRHNLWE
ESKQYCTDMNATLLKIDNRNIVEYIKARTHLIRWVGLSRQKSNEVWKWEDGSVISENMFEFL
EDGKGNMNCAYFHNGKMHPTFCENKHYLMCERKAGMTKVDQLP

100
90
80
70
60
50
40
30
20
10
0
100
90
80
70
60
50
40
30
20
10
0

FIGURE 307

CCCACGCGTCCGCGCAGTCTGCGCAGTTCTGCCTCCGCTGCCAGTCTCGCCCCGCGATCCCCG
 CCGGGGCTGTGGCGTGCAGTCCGACCCAGGCAGCCAGCAGCCCCGCGCGGGAGCCGACCCG
 CGCCGGAGGAGCTCGGACGGCATGCTGAGCCCCCTCCTTTGCTGAAGCCCGAGTGC GGAGAA
 GCCCCGGCAAACGCAGGCTAAGGAGACCAAAGCGGCGAAGTCTGCGAGACAGCGGACAAGCAG
 CGGAGGAGAAGGAGGAGGAGGCGAACCAGAGAGGGGCGAGAAAAGAAGCGGTGGTGGTGGG
 CGTCGTGGCCATGCGCGGGCTATCGCCAGCTCGCTCATCCGTGAGAAGAGGCAAGCCCGCG
 AGCGCGAGAAATCCAACGCCTGCAAGTGTGTGTCAGCAGCCCCAGCAAAGGCAAGACCAGCTGC
 GACAAAAACAAGTTAAATGTCTTTTCCCGGGTCAAACCTCTTCGGCTCCAAGAAGAGGCGCAG
 AAGAAGACCAGAGCCTCAGCTTAAGGGTATAGTTACCAAGCTATACAGCCGACAAGGCTACC
 ACTTGCAGCTGCAGGCGGATGGAACCATTTGATGGCACCAAAGATGAGGACAGCACTTACACT
 CTGTTTAACCTCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCT
 GTACTTGGCAATGAACAGTGAGGGATACCTGTACACCTCGGAACCTTTTACACCTGAGTGCA
 AATTCAAAGAATCAGTGTTTGAATAATTATTATGTGACATATTCATCAATGATATACCGTCAG
 CAGCAGTCAGGCCGAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAA
 CCATGTGAAGAAGAACAAGCCTGCAGCTCATTTTCTGCCTAAACCACTGAAAGTGGCCATGT
 ACAAGGAGCCATCACTGCACGATCTCACGGAGTTCTCCCGATCTGGAAGCGGGACCCCAACC
 AAGAGCAGAAGTGTCTCTGGCGTGCTGAACGGAGGCAAATCCATGAGCCCAATGAATCAAC
 GTAGCCAGTGAGGGCAAAGAAGGGCTCTGTAACAGAACCTTACCTCCAGGTGCTGTTGAAT
 TCTTCTAGCAGTCCTTCACCCAAAAGTTCAAATTTGTGAGTGACATTTACCAACAACAACAGG
 CAGAGTTCATATTCTATCTGCCATTAGACCTTCTTATCATCCATACTAAAGC

FIGURE 308

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA28498
><subunit 1 of 1, 245 aa, 1 stop
><MW: 27564, pI: 10.18, NX(S/T): 1
MAAAIASSLIRQKRQAREREKSNACKCVSSPSKGKTSCKNKNLVFSRVKLFSGSKRRRRRP
EPQLKGIVTKLYSRQGYHLQLQADGTIDGTDKEDSTYTLFNLIPVGLRVVAIQGVQTKLYLA
MNSEGILYTSELFTECKFKESVFENYYVTYSSMIYRQQQSGRGWYGLNKEGEIMKGNHVK
KNKPAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKRSVSGVLNGGKSMHNEST

N-glycosylation site.

amino acids 242-246

Glycosaminoglycan attachment site.

amino acids 165-169, 218-222

Tyrosine kinase phosphorylation site.

amino acids 93-100

N-myristoylation site.

amino acids 87-93, 231-237

ATP/GTP-binding site motif A (P-loop).

amino acids 231-239

HBGF/FGF family proteins

amino acids 78-94, 102-153

FIGURE 309

CCAGGATGGAGCTGGGGCCTGTATAGCCATATTATTGTTCTATGCTACTAGACATGGGGGGG
 ACTTGGTGA AAAAGGTATTATCCAGCCAGAGGGTCTGGGAGCCCTGTCTTACTGAACCTGGG
 CAACCTGGATATTCTGAGACATATTTTGGGGGGATTTCAGTGAAAAAGTGGGGGATCCCCCT
 CCATTTAGAGTGTAGCAAAGGAAAAACACCAAGGTTGGGTTCCCTCCTGACATTGGCAGTG
 CCCAGTAGGGGTGGGATGAGCGAATATTCCCAAAGCTAAAGTCCCACACCCTGTAGATTAC
 AAGAGTGGATTGGCAGGAGTGTGCCCAAATACAGTGGAAGGTGCCTGAAGATATTTAA
 ACCACGCTCTGGAAATTTAGTGGGTCTTGCTTTGGGATAGGTGAAGTGAAGACAGACACTG
 GAGAGGAGGGAAGGGGACGTTTTCAATAGGAGGCAAAACTCGAGGGTGGGATCCACTGAGG
 AGTACATAGGCTGCTGGATCTGGTGGAGCCAGCACTGGGCCACGGGTGGTAACCTGGCTGCT
 GTGAGGGGGGTACGTGAGGGGGGGGTCTGGGGCTTATCCTCAGGTCCGTGGGTGGGGCAG
 CGAGTCGGGGCCTGAGCGTCAAGAGCATGCCCTAGTGAGCGGGCTCCTCTGGGGAGCCAG
 CGCGCTCCGGGCGCCTGCCGTTTGGGGGTGCTCCTCCCGGGGCGCTATGCGCGCGCTGGC
 CAGTAGCCTGATCCGGCAGAAGCGGGAGGTCCGCGAGCCCGGGGGCAGCCGGCCGCTGTCCG
 CGCAGCGGCGCTGTGTCCCCGCGGCACCAAGTCCCTTTGCCAGAAGCAGTCTCATCTG
 CTGTCCAAGGTGCGACTGTGCGGGGGGCGGCCGCGCGGCCGACCGCGGCCCGAGCCTCA
 GCTCAAAGGCATCGTCACCAAAGTGTCTGCCGCCAGGGTTTCTACCTCCAGGCGAATCCCG
 ACGGAAGCATCCAGGGCACCCAGAGGATACCAGTCTCCTCACCCTTCAACCTGATCCCT
 GTGGGCCCTCCGTGTGGTCACCATCCAGAGCGCCAAGCTGGGTCACTACATGGCCATGAATGC
 TGAGGGACTGCTCTACAGTTCGCCGCAATTCACAGCTGAGTGTGCTTTAAGGAGTGTGTCT
 TTGAGAATTACTACGTCTGTACGCCCTCTGCTCTTACCGCCAGCGTCTGTTCTGGCCGGGCC
 TGGTACCTCGGCCTGGACAAGGAGGGCCAGGTCATGAAGGGAAACCGAGTTAAGAAGACCAA
 GGCAGCTGCCACTTTCTGCCAAGCTCCTGGAGGTGGCCATGTACCAGGAGCCTTCTCTCC
 ACAGTGTCCCGAGGCGCTCCCTTCCAGTCCCCCTGCCCTCGAATATGAGTCCCTGGACTG
 GAGGTTCCCTGCACTCCAGTGAGCCAGCCACCACCACAACCTGT

FIGURE 310

MAALASSLIRQKREVREPGGSRPVSAQRRVCPRGTSKSLCQKQLLILLSKVRLCGGRPARPDR
GPEPQLKGIVTKLFCRQGFYLQANPDGSIQGTPEDTSSFTHTFNLI PVGLRVVTIQSAKLGHY
MAMNAEGLLYSSPHFTAECRFKECVFENYYVLYASALYRQRRSGRAWYLGLDKEGQVMKGNR
VKKTAAAHLFLPKLLEVAMYQEPSLHSVPEASPSSPPAP

Tyrosine kinase phosphorylation site:

amino acids 199-207

N-myristoylation sites:

amino acids 54-60, 89-95, 131-137

HBGF/FGF family signature:

amino acids 131-155

FIGURE 311

ATGGCCGCGGCCATCGCTAGCGGCTTGATCCGCCAGAAGCGGCAGGCGCGGGAGCAGCACTG
GGACCGGCGCTCTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACC GCGGGCTCTGCAACG
GCAACCTGGTGGATATCTTCTCCAAAGTGC GCATCTTCGGCCTCAAGAAGCGCAGGTTGCGG
CGCCAAGATCCCAGCTCAAGGGTATAGTGACCAGGTTATATTGCAGGCAAGGCTACTACTT
GCAAAATGCACCCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACACTCT
TCAACCTCATACCAAGTGGGACTACGTGTTGTTGCCATCCAGGGAGTGAAAACAGGGTTGTAT
ATAGCCATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTACCCTGAATGCAAGTT
TAAAGAATCTGTTTTTGAAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGG
AATCTGGTAGAGCCTGGTTTTTGGGATTAAATAAGGAAGGGCAAGCTATGAAAGGGAACAGA
GTAAAGAAAACCAAACCAGCAGCTCATTTTCTACCCAAGCCATTGGAAGTTGCCATGTACCG
AGAACCATCTTTGCATGATGTTGGGAAACGGTCCCGAAGCCTGGGGTGACGCCAAGTAAAA
GCACAAGTGCCTCTGCAATAATGAATGGAGGCAAACCAAGTCAACAAGAGTAAGACAACA**TAG**

FIGURE 312

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA28503

><subunit 1 of 1, 247 aa, 1 stop

><MW: 27702, pI: 10.36, NX(S/T): 2

MAAAIASGLIRQKRQAREQHWRPSASRRRSSPSKNRGLCNGNLVDIFSKVRIFGLKKRRLR
 RQDPQLKGIVTRLYCRQGYLQMHPDGALDGTKDDSTNSTLFNLIPVGLRVVAIQGVKTGLY
 IAMNGEGYLYPSELTPECKFKESVFENYYVIYSSMLYRQQESGRAWFLGLNKEGQAMKGNR
 VKKTKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASAIMNGGKPVNKSSTT

N-glycosylation site.

amino acids 100-104, 242-246

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 28-32, 29-33

Tyrosine kinase phosphorylation site.

amino acids 199-207

N-myristoylation site.

amino acids 38-44, 89-95, 118-124, 122-128, 222-228

HBGF/FGF family proteins.

amino acids 104-155, 171-198

FIGURE 313

GGGGAGAGGAATTGACCATGTAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTTGGGTGCTTGCAAAAAAT
 GAAGGATGCAGGAGCGACCTTTCTCCTGGAAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAAGGAAGA
 ACGAAGCTTTTTCTGTGAGCCCTGGATCTTAACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAAATG
 AAATAAACCCAGAGTTAGACCCGCGGGGGTTGGTGTGTTCTGACATAAAATAAATACTTTAAAGCAGCTGTTCCC
 CTCCCCACCCCCAAAAAAGGATGATTGGAATGAAGAACCGAGGATTACAAAGAAAAAAGTATGTTTCATT
 TTCTCTATAAAGGAGAAAGTGACCCAGGAGATATTTTGGAAATGAAAAGTTTGGGGCTTTTTTGTAGTAAGTAA
 AGAACTGGTGTGGTGGTGTTCCTTTCTTTTTGAATTTCCCAAGAGGAGGAGAAATTAATAATACATCTGC
 AAGAAATTTAGAGAAAGAAAGTTGACCGCGCAGATTGAGGCATTGATTGGGGAGAGAAACACAGAGAGCA
 CAGTTGGATTTTGGCTATGTTGACTAAAATGACGGATAATGACAGTTGGATTTTCTTCATCAACCTCCTTT
 TTTTAAATTTTATTCCTTTTGGTATCAAGATCATCGCTTTTCTCTGTTCTTAACCACTGGATTTCATCT
 GGATGTTGCTGTGATCAGTCTGAAATACAACCTGTTTGAATTCAGAAAGGACCAACACAGATAAAATATGAATG
 TTGAACAAGATGACCTTACATCCACAGCAGATAATGATAGGCTCCTAGGTTTAAACAGGGCCCTATTTGACCCCT
 GCTTGTGGTGTCTGCTGGCTCTTCAACTTCTTGTGGTGGCTGCTGTGGTGCGGGCTCAGACCTGCCCTCTGTGT
 GCTCCTGCAGCAACCACTGTCAGCAAGTGATTGTTGTTCCGAAAAACCTGCGTGAAGTTCCGGATGGCATCTCC
 ACCAACACACGGCTGCTGAACCTCCTATGAGAACCAATCCAGATCATCAAAGTGAACAGCTTCAAGCACTTGAG
 GCACTTGGAAATCCTACAGTTGAGTAGGAACCATACGAACCATGAAATGGGGCTTTCAATGCTCTGGCGA
 ACCTCAACACTCTGGAACCTTTTGACAACTGCTTACTACCATCCCGAATGGAGCTTTTGTATACTTGTCTAAA
 CTGAGAGGAGCTCTGTTTGGCAAAACACCCCATGAAAGCATCCCTTCTTATGCTTTTAAACAGAAATCCTTCTTT
 GCGCGCACTAGACTTAGGGGAATGAAAAGACTTTATACATCTCAGAAAGTGCCCTTGAAGGTCTGTCCAACCT
 TGAGGATTTTGAAGCTTGCATGTGCAACCTTCGGGAAATCCCTACCTCAGCCGCTCATAAAACTAGATGAG
 CTGGATCTTTCTGGGAATCATTTATCTGCCATCAGGCCCTGGCTCTTTCCAGGGTTTATGACACCTTCAAAAACT
 GTGGATGATACAGTCCCAGATTCAAGTGATTGAACGGAATGCCTTTGACAACTTCAGTCACTAGTGGAGATCA
 ACCTGGCACAAATAATCTAACATTACTGCCTCATGACCTCTTCACTCCCTTGCATCATCTAGAGCGGATACAT
 TTACATCAACACCTTGGAACTGTAACCTGTGACATCTGTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTC
 GAACACAGCTTGTGTGCCCGGTGTAACACTCCTCCCAATCTAAAGGGAGGTACATTGAGAGCTCGACCAGA
 ATTACTTCACATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGCAGCT
 GAGCTGAAATGTGGGCTCCACATCCCTGACATCTGTATCTTGGATTACTCCAAATGGAACAGTATGACACA
 TGGGGCGTGAAGAATGCGGATAGCTGTGCTCAGTGTGAGTACGTTAAATTTCAAAATGTAACCTGTGCAAGATA
 CAGGCGATGTACATGTATGTTGAGTAATTCGTTGGGAATACTACTGCTTCAGCCACCCCTGAATGTACTGCA
 GCAACCACTACTCCTTTCTTCTTACTTTTCAACCGTCAAGTAGAGACTATGGAACCGTCTCAGGATGAGGCAG
 GACCACAGATAAACAATGTGGGTCCCACTCCAGTGGTCACTGGGAGACCAACAATGTGACCACTCTCTCACAC
 CACAGAGCACAAAGTCGACAGAGAAACCTTCACCATCCAGTGACTGATATAAACAGTGGGATCCCGGAAT
 GATGGGTGATGAAGACTACCAAAATCATCTATTGGGTGTTTGTGGCCATCACACTCATGGCTGCAGTGATGCT
 GGTCAATTTTCTACAAGATGAGGAAGCAGCACCATCGGCAAAACCATCAGCCCCAACAGGACTGTTGAAATTA
 TTAATGTGGATGATGAGATTACGGGAGACACACCCATGGAAGGCCACTGCCATGCTGCTATCGAGCATGAG
 CACCTAAATCACTATAACTCATACAAATCTCCCTTCAACCAACACAACAGTTAAACAAATAAATCAATACA
 CAGTTCAGTCATGAACCGTTATGTATCCGAATGAACCTTAAAGACAAATGTACAAGAGACTCAAATCTAAACA
 TTTACAGAGTTACAAAAACAACAATCAAAAAAAGACAGTTTATAAAAATGACCAAAATGACTGGGCTAA
 ATCTACTGTTTCAAAAAAGTGCTTTTCAAAAAAACAACAAAGAAATTTATTTATTAATAAATCTATTG
 TGATCTAAAGCAGACAAAAA

FIGURE 314

MLNKMTLHPQQIMIGPRFNRALFDPLLVLALLQQLLVVAGLVRAQTCPSVCSCSNQFSKVIC
VRKNLREVDPDGISTNTRLNLHENQIQIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
NLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS
YISEGAFEGLSNLRYLNLAMCNLREIPNLTPLIKLDLDELDSGNHLSAIRPGSFQGLMHLQKL
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLPLHDLFTPLHHLERIHLLHNPWNCNDIL
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE
LKCRATSLTSVSWITPNGTVMTHGAYKVRIVASDGTINFTNVTVDQDTGMYTCMVNSVGN
TTASATLNVTAATTTFFSYFSTVTVTETMEPSQDEARTDNNVGPTPVVDWETTNVTTSLTPQ
STRSTKFTFTIPVTDINSIGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN
HHAPTRTVEIINVDDIEITGDTPMESHLPMPAIEHEHLNHYSYKSPFNHTTTVNTINSIHSS
VHEPLLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419,
434-438, 442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

FIGURE 315

GCGCCGGGAGCCCATCTGCCCCAGGGGCACGGGGCGCGGGGCGGCTCCCGCCGGGCACAT
 GGCCTGAGCCACCTCGCGCGCACCCCGAGGCGCCGCGCCAGCTCGCCCGAGGTCCGTCGGA
 GCGCGCCCGCGCCCGCGGAGCCAAGCAGCAACTGAGCGGGGAAGCGCCCGCTCCGGGGAT
 GGG**ATG**TCCCTCCTCTCTCTCTTGTCTAGTTTCTACTATGTTGGAACCTTGGGGACTCA
 CACTGAGATCAAGAGAGTGGCAGAGGAAAAGGTCACTTTGCCCTGCCACCATCAACTGGGGC
 TTCCAGAAAAGACACTCTGGATATTGAATGGCTGCTCACCATAATGAAGGGAAACAAAAA
 GTGGTGATCACTTACTCCAGTCGTCATGTCTACAATAACTTGACTGAGGAACAGAAGGGCCG
 AGTGGCCTTTGCTTCCAATTTCTTGGCAGGAGATGCCCTCTTGCAGATTGAACCTCTGAAGC
 CCAGTGATGAGGGCCGGTACACCTGTAAGGTTAAGAATTCAGGGCCCTACGTGTGGAGCCAT
 GTCATCTTAAAAGTCTTAGTGAGACCATCCAAGCCCAAGTGTGAGTTGGAAGGAGAGCTGAC
 AGAAGGAAGTGACCTGACTTTGCAGTGTGAGTCATCCTCTGGCACAGAGCCCATTTGTGTATT
 ACTGGCAGCGAATCCGAGAGAAAAGAGGAGGATGAACGTCTGCCTCCCAAATCTAGGATT
 GACTACAACCCACCTGGACGAGTTCTGCTGCAGAATCTTACCATGTCTTACTCTGGACTGTA
 CCAGTGCACAGCAGGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTGCGAGTAAGCTGTACAGT
 ATGTACAAAGCATCGGCATGGTTGCAGGAGCAGTGACAGGCATAGTGGCTGAGGCCCTGCTG
 ATTTTCCTCTTTGGTGTGGCTGCTAATCCGAAGGAAAGACAAAGAAAGATATGAGGAAGA
 GAGACCTAATGAAATTCGAGAAGATGCTGAAGCTCCAAAAGCCCGTCTTTGTGAAACCCAGCT
 CCTCTTTCCTCAGGCTCTCGGAGCTCACGCTCTGGTTCTTCTCCACTCGCTCCACAGCAAA
 AGTGCCCTCACGCGAGCCAGCGGACACTGTCAACTGACGCAGCACCCCGAGCCAGGGCTGGCCAC
 CCAGGCATACAGCCTAGTGGGGCCAGAGGTGAGAGGTTCTGAACCAAAGAAAGTCCACCATG
 CTAATCTGACCAAAGCAGAAACCCACCCAGCATGATCCCCAGCAGACGAGAGCCCTTCCAA
 ACGGTCT**CGA**ATTACAATGGACTTGACTCCCACGCTTTTCTAGGAGTCAGGGTCTTTGGACTC
 TTCTCGTCATTGGAGCTCAAGTCACCAGCCACACAACCAGATGAGAGGTCTATCAAGTAGCA
 GTGAGCATTGCACGGAACAGATTCAGATGAGCATTTCCTTTATACAATACCAACAAGCAAA
 AGGATGTAAGCTGATTCATCTGTAAAAAGGCATCTTATTGTGCCTTTAGACCAGAGTAAGGG
 AAAGCAGGAGTCCAAATCTATTGTTGACCAGGACCTGTGGTGAGAAGGTTGGGGAAAGGTT
 AGGTGAATATACCTAAAACCTTTTAATGTGGGATATTTTGTATCAGTGCTTTGATTACAAAT
 TTCAAGAGGAAATGGGATGCTGTTTGTAAATTTCTATGCATTTCTGCAAACTTATTGGATT
 ATTAGTTATTGAGACAGTCAAGCAGAACCACAGCCTTATTACACCTGTACACCATGTAC
 TGAGCTAACCACTTCTAAGAAACTCCAAAAAGGAAACATGTGTCTTCTATTCTGACTTAAC
 TTCATTGTCTATAAGGTTTGGATATTAAATTCAGGGGAGTTGAAATAGTGGGAGATGGAGA
 AGAGTGAATGAGTTTCTCCACTCTATACTAATCTCACTATTGTATTGAGCCCAAAATAAC
 TATGAAAGGAGACAAAAATTTGTGACAAAGGATTGTGAAGAGCTTTCCATCTTCATGATGTT
 ATGAGGATTGTTGACAAACATTAGAAATATATAATGGAGCAATTTGGGATTTCCCTCAAAAT
 CAGATGCCCTTAAGGACTTTCTGCTAGATATTCTGGAAGGAGAAATACAACATGTCATT
 TATCAACGCTCTTAGAAAGATTCTTCTAGAGAAAAAGGATCTAGGAATGCTGAAAGATTA
 CCCAACATACCATTATAGTCTCTTCTTCTGAGAAAAATGTGAAACCAGAATTGCAAGACTGG
 GTGGACTAGAAAGGGAGATTAGATCAGTTTCTCTTAATATGTCAAGGAAGGTAGCCGGGCA
 TGGTGCCAGGCACCTGTAGGAAAAATCCAGCAGGTGGAGGTTGCAGTGAGCCGAGATTATGCC
 ATTGCACTCCAGCCTGGGTGACAGAGCGGGACTCCGCTCTC

FIGURE 316

>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLVSYVGTGLGTHTEIKRVAEEKVTLPCHHQGLPEKDTLDIEWLLTDNEGNQKV
 VITYSSRHVYNNLTTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCVKNSGRYVWSHV
 ILKVLVRPSKPKCELEGELTEGSDLTLCCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID
 YNHPGRVLLQNLTMSYSGLYQCTAGNEAGKESCVVRVTQYVQSIGMVAGAVTGIVAGALLI
 FLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSGSRSSRSGSSSTRSTANS
 ASRSQRTLSTDAAPQPLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFAQTV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 232-251



FIGURE 317

CGCGAGGCGCGGGAGCCTGGGACCAGGAGCGAGAGCCGCTACCTGCAGCGCGCGCCACGGCAGCGCAGCCA
 CCATGGCGGCTCTGCTGTGCTTCCTGCTCCTGCGGAGTAGTGGATTTCGCCAGAAATTTGAGTATCACTACT
 CCTGAGAGATGATTGAAAAAGCCAAAGGGGAAACTGCCATTGCCATGCAAAATTTACGCTTAGTCCCGAAGA
 CCAGGGACCGCTGGACATCGAGTGGCTGATATCACCAGCTGATAATCGAAGTGGGATCAAGTGATTATTTTAT
 ATTCTGGAGACAAAAATTTATGATGACTACTATCCAGATCTGAAAGGCCGGAGTACATTTTACGAGTAAATGATCTC
 AAACTCGTGATCATCATAAATGTAACGAATTTACAAGTCTCAGATATTTGGCACATATCAGTGCAGAAAGTAA
 AAAAGCTCCTGGTGTGCAAAATAGAGAGATTCACTGGTAGTTCTTGTAAAGCCTTCAGGTGCGAGATGTTACG
 TTGATGGATCTGAAGAAATGGAGGTGACTTTAAGATAAAATGTGAACCAAAGAGGTTTCATCTCCATTACAG
 TATGATGGCAAAATTTGCTGACTCACGAAAAATGCCACTTCATGGTTAGCAGAAATGACTTCATCTGTTAT
 ATCTGTAAGAAATGCCCTCTCTGAGTACTCTGGGACATACAGCTGTACAGTCAGAAACAGAGTGGGCTCTGATC
 AGTGCCTGTTGCGTCTAAACGTTGTCCTCTCTCAAAATAAGCTGGACTAATTCAGGAGCCATTATAGGAACT
 TTGCTTGCTCTAGCGCTCATTTGGTCTTATCATCTTTTGTCTGCTGTAAGAGCGCAGAGAAGAAAAATATGAAAA
 GGAAGTTCATCAGATATCAGGGAAGATGTGCCACTCCAAAGAGCCGTACGTCACCTGCCAGAAAGTACATCG
 GCAGTAATCATTTCCTCGGGGTCATGTCTCTTCCAACATGGAAGGATATTCGAAGACTCAGTATAACCAA
 GTACCAAGTGAAGACTTTGAACCACTCTCAGAGTCCGACTCTCCACCTGCTAAGTTCAGTACCCCTACAA
 GACTGATGGAATTACAGTTGATTAATATGGACTACTGAAGAATCTGAAGTATTGTATTATTTGACTTTATTTT
 AGGCCCTCTAGTAAAGACTTAAATGTTTTTAAAAAAAGCACAGGCGACAGAGATTAGAGCAGCTGTAAGAACAC
 ATCTACTTTATGCAATTGGCATTAGACATGTAAGTCAGATGTCAATGTCAAATTAGTACGAGCCAAATTTCTTGT
 TAAAAAACCCCTATGTATAGTGACACTGATAGTTAAAGATGTTTTATTATATTTTCAATACTACCACATACAA
 ATTTTTAACTTTTCATATGCATATTTCTGATATGGTCTTTTAGGAAAAGTATGGTTAATAGTTGATTTTTTCAA
 AGGAATTTTAAATTTCTTACGTTCTGTTTAAATGTTTTGCTATTAGTTAAATACATTTGAAGGGAATACCCG
 TTCTTTTCCCTTTTATGCACACAAAGAAACAGCGGTTGCTATGCCCTCAAATTTTTTTATTATTCACAACTACA
 TGATTTTACACAAATCTCTTAAACAAACGACATAAAATAGATTTTCTTGTATTAATAACTACATACAGCTTCAA
 TAAAGTAAATTTCAAAGGTTCTAGAACAAATCGTCCACTCTACAGTGTCTCGTATCCACACAGAGTTGATGC
 ACAATATATAAATCTCAAGTCCAATATTAATAAATCTAGGCACTTGACTAACTTAAATAAATTTTCTCAAACATA
 TATCAATATCTAAGTGATATATTTTTTAAGAAAGATTATCTCAATAACTTCTATAAAAAATAGATTGTATGG
 TTTGGCCCTCACTAACTTCACTATTAATTAAGAACTTTTAACTTTAATGTTCTAGTAAAGTTTATTCTAAGTT
 TTTCTCAACATGACACCAACACATCAAAACGAAGTTAGTGAGTGTCAACATCTGAGGATTAATCCAGTGAT
 TCCGCTCACATGCATCCAGAGGAGGTACCCATGTCACCTGGAATTTGGGCGATATGGTTTATTTTCTCTCCC
 TGATTTGGATTAACCAAATGGAACAGGAGGATAGTATCTGATGGCCATTCCCTCGATACATCTCTGGCTT
 TTTTCTGCGCAAGGCTGCCACATTGGAAGAGTGGAAATATAAGTTCTGAAATCTGTAGGGAAGAGAACACAT
 TAAGTTAATTCAAAGGAAAAAATCATCATCTGTTCCAGATTCTCATTAAGACAAAGTTACCCACAACACT
 GAGATCACTCATAGTGACACTCCTATTGTCAAGTCTAATAACATTAACAACTCATGTGTAATAGGCGTATAA
 TGTATACAGGTTGACCAATGTTTTCTGAATGCATAAAGAAATGAATAACTCAACACAGTACTCTCTAAACAA
 CTTCAACCAAAAAAGCCAAACATGGAACGAATGGAAGCTTGTAAAGGACATGCTTTGTTTATGCTCAGTGGTTT
 CCACAGCTGGCTGACCCAGGAGTCACTTGGAGGCTTTAAATACAAAACATTTGGAGCTGGAGGCCATTATCCTT
 AGCAAGCTAATGCAGAAAGACAGAAATCACTACCGCATGTCTCACTTATAAGTGGGAGGTAAATGATAAGGAT
 TATGAACACAAAGGAAGAAACAAATAGACATTTGGAGCTTATTTGAGAGGGGAGGGTGGGAGAGGAAAGGAGCA
 GAAAGATAACTATTGTAGTACTGCCTTACACCTGGGTGATGAAATTAATGTACAAACAAATCCCTGTGACACA
 TGTTTACCTATGGAACAACCTTCATGTGTATCCTTAAACCTTAAATTAAGGTAAAAAAGGAAAAAAGGAAAAA
 AAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAA
 AAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAA

FIGURE 318

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA82361

><subunit 1 of 1, 352 aa, 1 stop

><MW: 38938, pI: 7.86, NX(S/T): 3

MALLLCFVLLCGVVDFAFARSLSITTPPEEMIEKAKGETAYLPCKFTLSPEDQGPLDIEWLISPA
DNQKVDQVIILYSGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVTLQLSDIGTYQCKVKK
APGVANKKIHLLVVLVKPSGARCYPVDGSEEIGSDFKIKCEPKESLPLQYEWQKLSDSQKMPT
SWLAEMTSSVISVKNASSEYSGTYSCTVRNRVGSQDQCLLRNLNVPPSPNKAGLIAGAIIGTLL
ALALIGLIIFCCRKKRREEKYEKEVHHDIREDVPPPKSRTSTARSYIGSNHSSLGSMSPSNM
EGYSKTQYNQVPSSEDFERTPQSPTLPPAKFKYPYKTDGITVV

Signal sequence.

amino acids 1-19

Transmembrane domain:

amino acids 236-257

N-glycosylation sites.

amino acids 106-110, 201-205, 298-302

Tyrosine kinase phosphorylation sites.

amino acids 31-39, 78-85, 262-270

N-myristoylation sites.

amino acids 116-122, 208-214, 219-225, 237-243, 241-247,
245-251, 296-302

Myelin P0 protein.

amino acids 96-125

FIGURE 319

TGAATGACTTCCACGGCTGGGACGGGAACCTTCCACCCACAGCTATGCCTCTGATTGGTGA
 ATGGTGAAGGTGCTGTCTAATTTTCTGTAAAAAGAACAGCTGCCTCCAGGCAGCCAGCC
 CTC AAGCATCACTTACAGGACCAGAGGGACAAGACATGACTGTGATGAGGAGCTGCTTTCGC
 CAATTTAACACCAAGAAGATTGAGGCTGCTTGGGAGGAAGGCCAGGAGGAACACGAGACTG
 AGAGATGAATTTTCAACAGAGGCTGCAAAGCCTGTGGACTTTAGCCAGACCCTTCTGCCCTC
 CTTTGCTGGGCACAGCCTCTCAAATGCAGATGGTTGTGCTCCCTTGCCCTGGGTTTTACCCTG
 CTTCTCTGGAGCCAGGTATCAGGGGCCAGGGCCAAGAATTCCACTTTGGGCCCTGCCAAGT
 GAAGGGGGTTGTTCCCCAGAACTGTGGGAAGCCTTCTGGGCTGTGAAAGACACTATGCAAG
 CTCAGGATAACATCAGAGTGCCCGGCTGCTGCAGCAGGAGGTTCTGCAGAACGTCTCGGAT
 GCTGAGAGCTGTTACCTTTGTCCACACCCTGCTGGAGTTCTACTTGAAAAGTGTTCCTCAAAAA
 CCACCACAATAGAACAGTTGAAGTCAGGACTCTGAAGTCATTCTCTACTCTGGCCAACAAC
 TTGTTCTCATCGTGTCAAACTGCAACCCAGTCAAGAAAATGAGATGTTTTCCATCAGAGAC
 AGTGACACACAGGCGGTTTCTGCTATTCCGGAGAGCATTCAAACAGTTGGACGTAGAAGCAGC
 TCTGACCAAAGCCCTTGGGGAAGTGGACATTCTTCTGACCTGGATGCGAAAATCTACAAGC
 TCTGAATGTCTAGACCAGGACCTCCCTCCCCCTGGCACTGGTTTGTTCCTGTGTCAATTCA
 AACAGTCTCCCTTCCTATGCTGTTCACTGGACACTTCACGCCCTTGGCCATGGGTCCCATTCT
 TTGGCCAGGATTATGTCAAAGAAGTCATTCTTTAAGCAGCGCCAGTGACAGTCAGGGAAG
 GTGCCCTCTGGATGCTGTGAAGAGTCTACAGAGAAGATTCTGTATTTATTACAACCTCTATTT
 AATTAATGTCAGTATTTCAACTGAAGTCTATTTATTTGTGAGACTGTAAGTTACATGAAGG
 CAGCAGAATATGTGCCCCATGCTTCTTTACCCCTCACAATCCTTGCCACAGTGTGGGGCAG
 TGGATGGGTGCTTAGTAAGTACTTAATAAACTGTGGTGCTTTTTTTGGCCTGTCTTTGGATT
 GTTAAAAAACAGAGAGGGATGCTTGGATGTAAAAGTGAAGTTCAGAGCATGAAAATCACACT
 GTCTTCTGATATCTGCAGGGACAGAGCATTGGGGTGGGGGTAAAGTGCATCTGTTTGAAAAG
 TAAACGATAAAATGTGGATTAAAGTGCCAGCACAAAGCAGATCCTCAATAAACATTTTCATT
 TCCCACCCACACTCGCCAGCTCACCCCATCATCCCTTTCCCTTGGTGCCCTCCTTTTTTTTTT
 TATCCTAGTCATTCTTCCTAATCTTCCACTGAGTGTCAAGCTGACCTTGCTGATGGTGAC
 ATTGACCTGGATGTACTATCCAATCTGTGATGACATTCCTTGCTAATAAAAGACAACATAA
 CTC CAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 320

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA88002

><subunit 1 of 1, 206 aa, 1 stop

><MW: 23799, pI: 9.12, NX(S/T): 3

MNFQQRQLQSLWTLARFPCPLLATASQMVMVLPCLGFTLLLSQVSGAQGGQEFHFGPCQVK
 GVVPPQKLWEAFWAVKDTMQAQDNITSARLLQQEVLQNVSDAESCYLEVHTLLEFYKLTVFKNH
 HNRTVEVRTLKSFSTLANNFVLIVSQLQPSQENEMFSIRDSAHRRFLLFRRAFKQLDVEAAL
 TKALGEVDILLTWMQKFYKL

Signal sequence:

amino acids 1-42

N-glycosylation sites.

amino acids 85-89, 99-103, 126-130

FIGURE 321

AAGGAGCAGCCCGCAAGCACCAAGTGAGAGGCATGAAGTTACAGTGTGTTTCCCTTTGGCTC
 CTGGGTACAATACTGATATTGTGCTCAGTAGACAACCACGGTCTCAGGAGATGTCTGATTTCC
 CACAGACATGCACCATATAGAAGAGAGTTTCCAAGAAATCAAAGAGCCATCCAAGCTAAGG
 ACACCTTTCCCAAATGTCACTATCCTGTCCACATTGGAGACTCTGCAGATCATTAAGCCCTTA
 GATGTGTGCTGCGTGACCAAGAACCCTCCTGGCGTTCTACGTGGACAGGGTGTTCAAGGATCA
 TCAGGAGCCAAACCCCAAAATCTTGAGAAAAATCAGCAGCATTGCCAACTCTTTCCCTCTACA
 TGCAGAAAACTCTGCGGCAATGTCAGGAACAGAGGCAGTGTCACTGCAGGCAGGAAGCCACC
 AATGCCACCAGAGTCATCCATGACAACTATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA
 ATCCCTGGGAGAGCTCGACGTCTTTCTAGCCTGGATTAATAAGAATCATGAAGTAATGTTCT
 CAGCTTGATGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCCTGTGCGGTTTACT
 GTGGGAGACAGCCACCTTGAAGGGGAAGGAGATGGGAAGGCCCTTGCAGCTGAAAGTCC
 CACTGGCTGGCCTCAGGCTGTCTTATTCGCTTGAAAAATAGGCAAAAAGTCTACTGTGGTAT
 TTGTAATAAACTCTATCTGCTGAAAGGGCCTGCAGGCCATCCTGGGAGTAAAGGCTGCCTT
 CCCATCTAATTATTGTAAAGTCATATAGTCCATGCTGTGTGATGTGAGCCAAGTGATATCCT
 GTAGTACACATTGTACTGAGTGTTTTTCTGAATAAATCCATATTTTACCTATGA

1173
 1174
 1175
 1176
 1177
 1178
 1179
 1180
 1181
 1182
 1183
 1184
 1185
 1186
 1187
 1188
 1189
 1190
 1191
 1192
 1193
 1194
 1195
 1196
 1197
 1198
 1199
 1200

FIGURE 322

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282
><subunit 1 of 1, 177 aa, 1 stop
><MW: 20452, pI: 8.00, NX(S/T): 2
MKLQCVSLWLLGTILILCSVDNHGLRRCLISTDMHHIEESFQEIKRAIQAKDTFPNVTILST
LETLQIIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANSFLYMQKTLRQCQEQ
RQCHCRQEATNATRVIHNDNYDQLEVHAAAIKSLGELDVFLAWINKNHEVMFSA
```

Signal sequence:

amino acids 1-18

N-glycosylation sites.

amino acids 56-60, 135-139

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation site.

amino acids 24-30

Actinin-type actin-binding domain signature 1.

amino acids 159-169

FIGURE 323

CCCGTGCCAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCCCACTTGGCTTCGTTAG
 AACGCGGCTACAATTAATACATAACCTTATGTATCATACACATACGATTTAGGTGACACTAT
 AGAATAACATCCACTTTGCCTTTCTCTCCACAGGTGTCCACTCCCAGGTCCAAGTGCACCTC
 GGTTCATCGATAATCTCAGCACCAGCCACTCAGAGCAGGGCACGATGTTGGGGGCCCCGCT
 CAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCCTCAGAGCCTATCCCA
 ATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCC
 AGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGAC
 CATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGA
 TGAGCAGAAGATACCTCTGCATGGATTTTACAGGGCAACATTTTTGGATCACACTATTTTCGAC
 CCGGAGAACTGCAGGTTCCAAACACCAGACGCTGGAAAACGGGTACGACGTCTACCACTCTCC
 TCAGTATCACTTCCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCTTCCTGCCAGGCATGAACC
 CACCCCGTACTCCAGTTCCTGTCCCGGAGGAACGAGATCCCCCTAATTCACTTCAACACC
 CCCATACCACGCGCGGCACACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCCTGAACGT
 GCTGAAGCCCCGGGCCCGATGACCCCGCCCCGGCCTCCTGTTACAGGAGCTCCCGAGCG
 CCGAGGACAACAGCCCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGGCGGTGAGTGAAC
 ACGCACGCTGGGGGAACGGGCCCGGAAGGCTGCCGCCCTTCGCCAAGTTCATCTAGGGTTCG
 CTGG

FIGURE 324

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA142238
><subunit 1 of 1, 251 aa, 1 stop
><MW: 27954, pI: 9.22, NX(S/T): 1
MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNsyHLQIHKNGHVD
GAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENC RFQHQTLENGY
DVIHSPQYHFLVSLGRAKRAFLPGMNPPYPYSQFLSRRNEIPLIHFNTPIPRRHTRSAEDDSE
RDPLNLVKPRARMT PAPASCSQELPSAEDNSPMASDPLGVVRRGRVNT HAGGTGPEGCRPFA
KFI
```

Important features of the protein:**Signal peptide:**

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 175-179

N-myristoylation site.

amino acids 33-39, 100-106, 225-231, 229-235

HBGF/FGF family proteins

amino acids 73-124

FIGURE 325

GGAAAAGGTACCCGCGAGAGACAGCCAGCAGTTCTGTGGAGCAGCGGTGGCCGGCTAGC**ATG**
 GGCTGTCTCTGGGGTCTGGCTCTGCCCTTTTCTTCTCTGTCTGGGAGGTTGGGGTCTCTGG
 GAGCTCTGCAGGCCCGCAGCACC CGCAGAGCAGACTGCGATGACAACGGACGACACAGAAG
 TGCCCGCTATGACTCTAGCACCGGGCCACGCGCTCTGGAACTCAAACGCTGAGCGCTGAG
 ACCTCTTCTAGGGCCTCAACCCAGCGGCCCATTCAGAAGCAGAGACCAGGGGAGCCAA
 GAGAATTTCCCTGCAAGAGAGACCAGGAGTTTCACAAAAACATCTCCCACTTCATGGTGC
 TGATCGCCACCTCCGTGGAGACATCAGCCGCCAGTGGCAGCCCCGAGGGAGCTGGAATGACC
 ACAGTTCAGACCATCACAGGCAGTGATCCCGAGGAAGCCATCTTTGACACCTTTGCACCGA
 TGACAGCTCTGAAGAGGCAAGACACTCACAATGGACATATTGACATTGGCTCACACCTCCA
 CAGAAGCTAAGGGCCTGTCTCTCAGAGAGCAGTGCTCTTCCGACGGCCCCCATCCAGTCATC
 ACCCGCTCAGGGCCTCAGAGAGCAGCGCTCTTCCGACGGCCCCCATCCAGTCATACCCC
 GTCAGGGCCTCAGAGAGCAGCGCTCTTCCGACGGCCCCCATCCAGTCATACCCCGTCAT
 GGTCCCCGGGATCTGATGTCACTCTCCTCGCTGAAGCCCTGGTGACTGTCAAAACATCGAG
 GTTATTAATTGCAGCATCACAGAAATAGAAACAACAACCTCCAGCATCCCTGGGGCCTCAGA
 CATAGATCTCATCCCCACGGAAGGGGTGAAGGCCTCGTCCACCTCCGATCCACCAGCTCTGC
 CTGACTCCACTGAAGCAAAACACACATCACTGAGGTCCAGCCTCTGCCGAGACCTGTCC
 ACAGCCGGCACCACAGAGTCAGCTGCACCTCATGCCAGGTTGGGACCCCACTCCCACTAA
 CAGCGCCACAGAAAGAGAAGTGACAGCACC CGGGGCCACGACCTCAGTGGAGCTCTGGTCA
 CAGTTAGCAGGAATCCCTGGAAGAAACCTCAGCCCTCTCTGTTGAGACACCAAGTTACGTC
 AAAGTCTCAGGAGCAGCTCCGGTCTCCATAGAGGCTGGGTGAGCAGTGGGCCAAAACAACCTC
 CTTTGCTGGGAGCTCTGCTTCTCTACAGCCCTCGGAAGCCGCCCTCAAGAACTTCACCC
 CTTCAGAGACACCGACCATGGACATCGCAACCAAGGGGCCCTCCCCACCAGCAGGACCT
 CTTCTTCTGTCCCTCCGACTACAACCAACAGCAGCCGAGGGACGAACAGCACCTTAGCCAA
 GATCACAACCTCAGCGAAGACCACGATGAAGCCCCAACAGCCACGCCACGACTGCCCGGAC
 GAGGCCGACCACAGAC**G**TGA**G**TGCAGGTGAAAATGGAGGTTTCTCTCTCTGCGGCTGAGTG
 TGGCTTCCCCGGAAGACCTCACTGACCCAGAGTGGCAGAAAGGCTGATGCAGCAGCTCCAC
 CGGGAACCTCACGCCCACGCGCTCACTTCCAGGTCTCTTACTGCGTGTGAGGAGGGCTA
 ACGGACATAGCTGCAGCAGGCATGTCCCGTATGCCAAAAGAGGTTGCTGCCCTTAGCCTG
 GGCCCCCACCAGACAGCTGCAGCTGCGTTACTGTGCTGAGAGGTACCCAGAAGGTTCCCATG
 AAGGGCAGCATGTCCAAGCCCTAACCCAGATGTGGCAACAGGACCTCGCTCACATCCAC
 CGGAGTGATGTATGGGGAGGGGCTTCACTGTTCAGAGGTTGCTTGGACTCACCTTGG
 CACATGTTCTGTGTTTCACTAAAGAGAGACCTGATACCCATCTGTGTGCTTCCATCCTGCA
 TTAATAATCACTCAGTGTGGCCCAAAAAA

FIGURE 326

MGCLWGLALPLFFFCWEVGVSGSSAGPSTRADTAMTTDDTEVPAMTLAPGHALETQTLA
 ETSSRASTPAGPIPEAETRGAKRISFARETRSFTKTSPNFMVLIATSVETSAASGSPEGAGM
 TTVQITIGSDPEEAFDITLCTDDSSSEAKTLTMDILTAAHTSTEAKGLSSESSASSDGPHPV
 ITPSRASESSASSDGPHPVITPSRASESSASSDGPHPVITPSWSPGSDVTLLEALVITVNI
 EVINCSITEIETTSSIPGASDIDLIPTEGVKASSTSDPPALPDSTEAKPHITEVTASAETL
 STAGTTESAAPHATVGTPLPTNSATEREVTAPGATTLGALVTVSRNPLEETSALSIVETPSY
 VKVSGAAPVSIEAGSAVGKTTSFAGSSASSYSPSEAALKNFTPSETPTMDIATKGPFPTSRD
 PLPSVPPTTNNSSRGNTSLAKITTSAKTTMKPQQPRRLPGRGRPQT

N-glycosylation sites:

amino acids 252-256, 445-449, 451-455

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 84-90

Casein kinase II phosphorylation sites.

amino acids 37-41, 108-112, 131-135, 133-137, 148-152, 165-169,
 246-250, 254-258, 256-260, 269-273, 283-287, 333-337, 335-339,
 404-408, 414-418, 431-435

N-myristoylation sites.

amino acids 2-8, 19-25, 117-123, 121-127, 232-238, 278-284, 314-
 320, 349-355, 386-392, 397-403, 449-455

ATP/GTP-binding site motif A (P-loop).

amino acids 385-393

FIGURE 327

GCGGAGCATCCGCTGCGGTCTCGCCGAGACCCCGCGGGATTGCGCGGTCTTCCGCGGG
 GCGCGACAGAGCTGTCTCGCACCTGGATGGCAGCAGGGGGCGCGGGGTCTCTCGACGCCA
 GAGAGAAAATCTCATCATCTGTGCAGCCTTCTTAAAGCAAACTAAGACCAGAGGGAGGATTAT
 CCTTGACCTTTGAAGACCAAACTAAACTGAAATTTAAAAATGTTCTTCGGGGGAGAGGGAG
 CTTGACTTACACTTTGGTAATAATTTGCTTCTTGACACTAAGGCTGTCTGCTAGTCAGAATT
 GCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGACATCCAGTCATCTCTTTCTAAGGGAATC
 AGAGGCAATGAGCCCGTATATACTTCAACTCAGAAGACTGCATTAATTTCTTGCTGTTCAAC
 AAAAAACATATCAGGGGACAAGCATGTAACCTTGATGATCTTCGACACTCGAAAAACAGCTA
 GACAACCCAACTGCTACCTATTTTTCTGTCCCAACGAGGAAGCCTGTCCATTGAAACAGCA
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 TAGCCCATCATCACACAGATTATTCAAAGCCACCGATATCTCATGGAGAGACACACTTTCT
 CAGAAGTTTGGATCCTCAGATCACCTGGAGAACTATTTAAGATGGATGAAGCAAGTGCCCA
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 TAGCTCATCTGCTGCCTGAAAATGTGAGTGCGCTCCAGCTACGGTGGCAGTTGCTTCTCCA
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 TTCTGGGACTTCCAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTC
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 TCGTCTCTCTGGGTAGAATCCTTTCGGAATCACTCCGAGGAAACGTTACTCAAGACTGGAT
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FIGURE 328

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><subunit 1 of 1, 431 aa, 1 stop
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SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
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TDSKGSLETIPFTEISNLTNTGNVYNPTALSMNSVESSTMNKTASWEGREASFGSSSQGSV
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```

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

CTCCACCGGTGTCCAGCGCCAGAAATGCGGCTTCTGGTCTGCTATGGGGTTCGCTGCTGCT
CCCAGGTTATGAGACCCCTGGAGGGCCGACAGGAATACGCGGGTTCGAAGGGGACATCTGT
CCCTGCAGTGCACCTCAGGGAAGAGCTGAGGACCACCGGAAGTATGGTGTCAGGAAGGGT
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CGGAGACAGCAGGAAGACGAGAAGTTCTGGCTCTCAGCTTGACTCGGGAGAAAAGAGGCC
CTTCTCCAGGCCCCTAGGGGGACGTGATCTCGATGCTCCCTCCACACATCTGAGGAGGA
GCTGGGCTTCTCGAAGTTTGTCTCAGCGTAGGGCAGGAGGCCCTCTGGCCAGCCAGCAT
TAACGAGTATGGCTGGCTGGATCAGACCCGATTCCCGAAAGCTTTCCACTCAGCCCTCAGAG
TCAGCTGCGCCGACTCAGGGGCTCTCCACCCTCCCAAGGCTCTCTCTTGATGTTTCCA
GCCTGACCTAGAAAGCGTTTGTCAAGCCCTGGAGCCAGCAGCGGCTGGCCTTGCTCTCCGGCT
GAGACTGGGACATCCCTGATAGGTTTCACTCCCTGGGCAGATACCAAGGCTGCTTGACCTCA
GCAGGGCCAGACAAAGGCTCAGTGGATCTGGTCTGAGTTTCAATTGCCAGGAACCTGCTGGGC
CTCATGCGCAAGTGTGCGAGCCCTGGCCTTCTCTCCACTCAGACCGGAGCTTGTCTCCCTCCC
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FIGURE 330

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196

<subunit 1 of 1, 332 aa, 1 stop

<MW: 36143, pI: 5.89, NX(S/T): 1

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FPGPCCFPSPSPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQKGTGA EAPPLPG
TSQYGHERTSQYTGTSHP PATSP PAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSI PMVRI
LAPVLVLLSLLSAAGLIAFC SHLLLRKEAQQATETQRNEKEWLSRLTAE EKEAPSQAPEGD
VISMPPLHTSEEELGFSKFVSA

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 248-269

N-glycosylation site.

amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.

amino acids 104-113

Ig like V-type domain:

amino acids 13-128